

Group 4

- **SEQ 1 from 54-05A application (10/613,053) against the large genomic sequence from Brown Provisional No. 1 (60/305,026)**

Score = 1.640e+04 bits (8528), Expect = 0.0
 Identities = 8547/8554 (99%), Gaps = 1/8554 (0%)
 Strand=Plus/Minus

Query	1	ATTTAAATTTTATACTTAATATGTATTTAAACTCTCCAATGCAATAAGGGATATAAACAA	60
Sbjct	173987	ATTTAAATTTTATACTTAATATGTATTTAAACTCTCCAATGCAATAAGGGATATAAACAA	173928
Query	61	AAGGTATTCATAGATGTTATGTATTCGTACACCGATGTATTCGTATACCTTAAATATATG	120
Sbjct	173927	AAGGTATTCATAGATGTTATGTATTCGTACACCGATGTATTCGTATACCTTAAATATATG	173868
Query	121	TATACTTATGTATACATATACTTGTGTATTCGTACACCTTAAGTATTCGATGGGTTATGT	180
Sbjct	173867	TATACTTATGTATACATATACTTGTGTATTCGTACACCTTAAGTATTCGATGGGTTATGT	173808
Query	181	TGGTATTCGTATATTTTATGTATTTGTACACCTTATGTATACTTATGTATATGTACACCT	240
Sbjct	173807	TGGTATTCGTATATTTTATGTATTTGTACACCTTATGTATACTTATGTATATGTACACCT	173748
Query	241	TATGTATTTGTACATCTTAAGTATTAGATGAGTTATGTTGATATTCGTACACCTTATGTA	300
Sbjct	173747	TATGTATTTGTACATCTTAAGTATTAGATGAGTTATGTTGATATTCGTACACCTTATGTA	173688
Query	301	TTCGTACACCTTCTGTATACCTTAGGTATTCGTACACCTTAGGTATTTGTACACCTAAGG	360
Sbjct	173687	TTCGTACACCTTCTGTATACCTTAGGTATTCGTACACCTTAGGTATTTGTACACCTAAGG	173628
Query	361	TATTCGTACACCTTATGTATACTTATGTATACGTACACCTTATATATTCGAACACCTTAG	420
Sbjct	173627	TATTCGTACACCTTATGTATACTTATGTATACGTACACCTTATATATTCGAACACCTTAG	173568
Query	421	ATATTCGTACATCTTATGTATACGTATACTTATTTCTTGAGTTATAGTGAATTAGATTGT	480
Sbjct	173567	ATATTCGTACATCTTATGTATACGTATACTTATTTCTTGAGTTATAGTGAATTAGATTGT	173508
Query	481	ATTAAACGTTAGACATAGGGTTCCGGATTTATCCAAGGGTTCCAGATTGTTTCAGATTCT	540
Sbjct	173507	ATTAAACGTTAGACATAGGGTTCCGGATTTATCCAAGGGTTCCAGATTGTTTCAGATTCT	173448
Query	541	GGATTTACCCAATGGTTCTGGATTTACCCAAGGGTTCCGGATTTAGGATTCAAGGTTTAG	600
Sbjct	173447	GGATTTACCCAATGGTTCTGGATTTACCCAAGGGTTCCGGATTTAGGATTCAAGGTTTAG	173388
Query	601	AGTTTAGGATTTTAGGTTTAGTGTGTTTGTGATGATTTTTAATATTTAAGATAAATGTAG	660
Sbjct	173387	AGTTTAGGATTTTAGGTTTAGTGTGTTTGTGATGATTTTTAATATTTAAGATAAATGTAG	173328

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Query	661	ACAAATTTGTTCTTCCTACCATTTTGACAAAAAATGAAAGATCTATGTAGGTTTCCAAGT	720
Sbjct	173327	ACAAATTTGTTCTTCCTACCATTTTGACAAAAAATGAAAGATCTATGTAGGTTTCCAAGT	173268
Query	721	TTATTAAATTTACCCAGATTTATGAAAATTATCCATAAATTTATATAATTTTATGAATAA	780
Sbjct	173267	TTATTAAATTTACCCAGATTTATGAAAATTATCCATAAATTTATATAATTTTATGAATAA	173208
Query	781	TTTATCATTTATTTGGGTAAATTTCATAAATATGAAAGTTTCTTTTATGGGTCAAAATGT	840
Sbjct	173207	TTTATCATTTATTTGGGTAAATTTCATAAATATGAAAGTTTCTTTTATGGGTCAAAATGT	173148
Query	841	ATAATTTATTTCGGATTCTGGATTTACCCAAGGGTCCGGATTACCCAAGGATTCCAGAT	900
Sbjct	173147	ATAATTTATTTCGGATTCTGGATTTACCCAAGGGTCCGGATTACCCAAGGATTCCAGAT	173088
Query	901	TTAGGATTCATGGTTTAGAGTTTAGGAGTTTATGTTTAGTGTTTTGTTGATGATTTTAAA	960
Sbjct	173087	TTAGGATTCATGGTTTAGAGTTTAGGAGTTTATGTTTAGTGTTTTGTTGATGATTTTAAA	173028
Query	961	TATTTAAGATAAGAAGTTTATGCGAGAGAATTTGGTCAAACCTCAGGTTGAGTCTTAACCT	1020
Sbjct	173027	TATTTAAGATAAGAAGTTTATGCGAGAGAATTTGGTCAAACCTCAGGTTGAGTCTTAACCT	172968
Query	1021	CTTAAGACATAAAAAATCACTAGATACTTGACATGGAGGCACCAAATTATCCTATATTTTT	1080
Sbjct	172967	CTTAAGACATAAAAAATCACTAGATACTTGACATGGAGGCACCAAATTATCCTATATTTTT	172908
Query	1081	TGGACTTAATCTTGGTGTACCCCTAGAGTAAACCTTAAGGTTACCAACCAATAGAAATC	1140
Sbjct	172907	TGGACTTAATCTTGGTGTACCCCTAGAGTAAACCTTAAGGTTACCAACCAATAGAAATC	172848
Query	1141	ACTCATTTACAGTTGATATCTTTTAAAAAAGTAAACAAAATATTGTCGAGTTATATTAC	1200
Sbjct	172847	ACTCATTTACAGTTGATATCTTTTAAAAAAGTAAACAAAATATTGTCGAGTTATATTAC	172788
Query	1201	ATTTTTAAAATAAAAAATATTAAAAAATAAAAAATAATAATATATGCAAAAAAAGATTTT	1260
Sbjct	172787	ATTTTTAAAATAAAAAATATTAAAAAATAAAAAATAATAATATATGCAAAAAAAGATTTT	172728
Query	1261	TTAAAAAGATTTTAATTTTCGTCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCC	1320
Sbjct	172727	TTAAAAAGATTTTAATTTTCGTCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCC	172668
Query	1321	TTGGATAAATACTAAACCCTAAATTAAAAACATTAAACCATAATAGTATTTTTAAGATTT	1380
Sbjct	172667	TTGGATAAATACTAAACCCTAAATTAAAAACATTAAACCATAATAGTATTTTTAAGATTT	172608
Query	1381	AATGTTTTAGTGTTTAGTGTTTTTGATTTAGAATTTAGGATTATCCAAGTGTTTATGATT	1440
Sbjct	172607	AATGTTTTAGTGTTTAGTGTTTTTGATTTAGAATTTAGGATTATCCAAGTGTTTATGATT	172548

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Query	1441	TATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTAGGGTTTAGAGTTTAAAATTATCCAA	1500
Sbjct	172547	TATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTAGGGTTTAGAGTTTAAAATTATCCAA	172488
Query	1501	GGGTCTAGGGTATACCCAAGGGTTTAGGGTTAGGATTTAGGGTTAGGGTTTAGAATTT	1560
Sbjct	172487	GGGTCTATGGTATACCCAAGGGTTTAGGGTTAGGATTTAGGGTTAGGGTTTAGAATTT	172428
Query	1561	AGGGTTTAGGGTTTAGAGTTTAAAATTATCCAAGGGTTTAGGGTATACCCAAGGGTTTAG	1620
Sbjct	172427	AGGGTTTAGGGTTTAGAGTTTAAAATTATCCAAGGGTTTAGGGTATACCCAAGGGTTTAG	172368
Query	1621	GGTTTAGGATTTAGGGTTTAAAGTTTAGTGTTTTTTGACGATATTAAAAATAGTTTTCAA	1680
Sbjct	172367	GGTTTAGGATTTAGGGTTTAAAGTTTAGTGTTTTTTGACGATATTAAAAATAGTTTTCAA	172308
Query	1681	AAATTCATTTTTTGTAAACGGCTATTATTTTTTTTTTATATTTTATTTATTTTAAAAACAT	1740
Sbjct	172307	AAATTCATTTTTTGTAAACGGCTATTATTTTTTTTTTATATTTTATTTATTTTAAAAACAT	172248
Query	1741	AATATAACTTGACAATATTTTCTTTTCTTTTAAAAAAATATTAATTATGAAATACTTG	1800
Sbjct	172247	AATATAACTTGACAATATTTTCTTTTCTTTTAAAAAAATATTAATTATGAAATACTTG	172188
Query	1801	ATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTAGGGGTGAACCTAAGGATAACTCT	1860
Sbjct	172187	ATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTAGGGGTGAACCTAAGGATAACTCT	172128
Query	1861	ATTTTTTGGGGTGAAATAGCACTATAGCGGATATCTTTTTCAATAGATTATAAGCACGGC	1920
Sbjct	172127	ATTTTTTGGGGTGAAATAGCACTATAGCGGATATCTTTTTCAATAGATTATAAGCACGGC	172068
Query	1921	TCTACCTATGACTAATCAAGAACTTGGGATGATTGGAAATCTGCAGGTTGTACTCAATAT	1980
Sbjct	172067	TCTACCTATGACTAGTCAAGAACTTGGGATGATTGGAAATCTGCAGGTTGTACTCAATAT	172008
Query	1981	GGGATTATATTGGTTCTAACAAGTAGATATGATCCTTGAAAATTAAAGTTATTAGATCAG	2040
Sbjct	172007	GGGATTATATTGGTTCTAACAAGTAGATATGATCCTTGAAAATTAAAGTTATTAGATCAG	171948
Query	2041	TTCATCGTGAAAGGTGTAGGGTTTGTCAATTTTATTAACAAATTTGTCAATTCATTAACAA	2100
Sbjct	171947	TTCATCGTGAAAGGTGTAGGGTTTGTCAATTTTATTAACAAATTTGTCAATTCATTAACAA	171888
Query	2101	TTTTTGTCAATTTTATAAACATGAAAATTATAACGAATGCACTTTGCTGCCAGATCCCAAT	2160
Sbjct	171887	TTTTTGTCAATTTTATAAACATGAAAATTATAACGAATGCACTTTGCTGCCAGATCCCAAT	171828
Query	2161	TTGTCATTTTATTTTTGGGAAAAAATGTAGCATTTTCGTGAGTGTTTCTATTTTTGGCAA	2220
Sbjct	171827	TTGTCATTTTATTTTTGGGAAAAAATGTAGCATTTTCGTGAGTGTTTCTATTTTTGGCAA	171768

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Query	2221	AAACAAAAAGTGTGAGATCAATTTTGACCAAAAAAATGTAAGATTCACGTAGGTTTCC	2280
Sbjct	171767	AAACAAAAAGTGTGAGATCAATTTTGACCAAAAAAATGTAAGATTCACGTAGGTTTCC	171708
Query	2281	AAATTTATTAAATTTACCCAACCTATATTAAAATTAAATGTAGACAAATTTGTTTTCTGC	2340
Sbjct	171707	AAATTTATTAAATTTACCCAACCTATATTAAAATTAAATGTAGACAAATTTGTTTTCTGC	171648
Query	2341	CATTTTGGCAAAAAATGAAGGATCTATGAAGGTTTCCAAGTTTATTAAATTTACTCAGAT	2400
Sbjct	171647	CATTTTGGCAAAAAATGAAGGATCTATGAAGGTTTCCAAGTTTATTAAATTTACTCAGAT	171588
Query	2401	TTATGATAATTATCCATAAATTTACATAATTTTATGAATTATCATTTATTTGGGTAGATT	2460
Sbjct	171587	TTATGATAATTATCCATAAATTTACATAATTTTATGAATTATCATTTATTTGGGTAGATT	171528
Query	2461	TCATAAATATGAAAGTTTCTTTTATGAGTCAAAATGTATAATTTATTGGGTAACCTTCAT	2520
Sbjct	171527	TCATAAATATGAAAGTTTCTTTTATGAGTCAAAATGTATAATTTATTGGGTAACCTTCAT	171468
Query	2521	AAATTTTAGAATTTACATCGATTTTATATTAATTCGTATAGATTTATGTTGACTTTATAT	2580
Sbjct	171467	AAATTTTAGAATTTACATCGATTTTATATTAATTCGTATAGATTTATGTTGACTTTATAT	171408
Query	2581	ATGAAAAAATATGTATTATATTAAGTAGTTGCTCATATATGATTTTTAAATATTAAAT	2640
Sbjct	171407	ATGAAAAAATATGTATTATATTAAGTAGTTGCTCATATATGATTTTTAAATATTAAAT	171348
Query	2641	ATGATCCAAAAGTTTAAATGAATAAAGAATGTTTATGGAATTTACAAAAGTTAGTTGTTAA	2700
Sbjct	171347	ATGATCCAAAAGTTTAAATGAATAAAGAATGTTTATGGGATTTACAAAAGTTAGTTGTTAA	171288
Query	2701	AAGTTAGTGGGAAAAAATTATTTTTTATAGGCAAAGTGGATTTTGGGTCCACGAAATT	2760
Sbjct	171287	AAGTTAGTGGGAAAAAATTATTTTTTATAGGCAAAGTGGATTTTGGGTCCACGAAATT	171228
Query	2761	ACTTTTCCAACCTTGCCAAGTTTAAATAGGCAAAAAGGTTAAAAATGTCATAAATTTATTCT	2820
Sbjct	171227	ACTTTTCCAACCTTGCCAAGTTTAAATAGGCAAAAAGGTTAAAAATGTCATAAATTTATTCT	171168
Query	2821	CTCTCTACTAGGTTGCCCAATTGCCTAATATAAACTTGAGGTGGCCTATTTTTCTAATTC	2880
Sbjct	171167	CTCTCTACTAGGTTGCCCAATTGCCTAATATAAACTTGAGGTGGCCTATTTTCCTAATTC	171108
Query	2881	AAACTTAAAAGTTGCCCTTTCCCCTAATTGACCCATAAAAGAATGAAAGACATTTTCTT	2940
Sbjct	171107	AAACTTAAAAGTTGCCCTTTCCCCTAATTGACCCATAAAAGAATGAAAGACATTTTCTT	171048
Query	2941	TTCCAAATTACAATCCCTAGATAATTTTATTTTGTAGGTGCATTCCATCGGTTATGATTA	3000
Sbjct	171047	TTCCAAATTACAATCCCTAGATAATTTTATTTTGTAGGTGCATTCCATCGGTTATGATTA	170988

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Query	3001	CAGAATAGCTACGCTTCTCTATTGATTCTTATTGCGCCGTTGGTGACGTTTTCCATGGAA	3060
Sbjct	170987	CAGAATAGCTACGCTTCTCTATTGATTCTTATTGCGCCGTTGGTGACGTTTTCCATGGAA	170928
Query	3061	TCAAGTAGTGTTTTATCTCCTATCACTAACAACATATTCATAGATTTTGTTTATCACTTG	3120
Sbjct	170927	TCAAGTAGTGTTTTATCTCCTATCACTAACAACATATTCATAGATTTTGTTTATCACTTG	170868
Query	3121	TTCTGTGTTCCCTGATCATATACTTGACTCAGTTTCTGTGATTTTCATCAAGTTTTTGAGAA	3180
Sbjct	170867	TTCTGTGTTCCCTGATCATATACTTGACTCAGTTTCTGTGATTTTCATCAAGTTTTTGAGAA	170808
Query	3181	CAGAAGAAGCAAAAAAGAAAACGAGCAGAGCTGCTCTTACAATGTTTTAACCGTGAGTGA	3240
Sbjct	170807	CAGAAGAAGCAAAAAAGAAAACGAGCAGAGCTGCTCTTACAATGTTTTAACCGTGAGTGA	170748
Query	3241	TAAATTTATTTACATAAAAGTATTTTAAAAATAGATTTAATCAACCAATTTAATATATTA	3300
Sbjct	170747	TAAATTTATTTACATAAAAGTATTTTAAAAATAGATTTAATCAACCAATTTAATATATTA	170688
Query	3301	TTTTATATTTAGTTCATTTTTTTTTTGACATCTTTTATATTTAGTTTGAACACCTCTATT	3360
Sbjct	170687	TTTTATATTTAGTTCATTTTTTTTTTGACATCTTTTATATTTAGTTTGAACACCTCTATT	170628
Query	3361	TGAGTACAACATAGATTATAATGATAAATTTATAAAATAGCATAATTTTTTATTTTCATT	3420
Sbjct	170627	TGAGTACAACATAGATTATAATGATAAATTTATAAAATAGCATAATTTTTTATTTTCATT	170568
Query	3421	GTTTTATGATAAAATTCTAAATAACAATAATTATAATATTATTATATTACTAATTGCAAA	3480
Sbjct	170567	GTTTTATGATAAAATTCTAAATAACAATAATTATAATATTATTATATTACTAATTGCAAA	170508
Query	3481	AATTAATTAATACATTATTTTATAATAAATATTTAAAACGTTGGGTAGGATTTTGTTAGA	3540
Sbjct	170507	AATTAATTAATACATTATTTTATAATAAATATTTAAAACGTTGGGTAGGATTTTGTTAGA	170448
Query	3541	TTTTTTTCAACAAATTTTGTTATAGCTAAAATAAAATTCAAATGTATTGTTAAATTTGAT	3600
Sbjct	170447	TTTTTTTCAACAAATTTTGTTATAGCTAAAATAAAATTCAAATGTATTGTTAAATTTGAT	170388
Query	3601	TTTTTTTTTTTTTTGATTATTAAGATTTAATATAAATAAACATATATGTCATATTAAATAT	3660
Sbjct	170387	TTTTTTTTTTTTTTGATTATTAAGATTTAATATAAATAAACATATATGTCATATTAAATAT	170328
Query	3661	TTAACTAAGTGGTCCTAATCTTTGAACTAGGGGTGGGCGTTCGGGTACCTATTCGGGTTT	3720
Sbjct	170327	TTAACTAAGTGGTCCTAATCTTTGAACTAGGGGTGGGCGTTCGGGTACCTATTCGGGTTT	170268
Query	3721	CGGTTCGAGTCTATTCGGATTTTCGGATTTTGGGGTCAAAGATTTTAGCCCCATTCGGTT	3780
Sbjct	170267	CGGTTCGAGTCTATTCGGATTTTCGGATTTTGGGGTCAAAGATTTTAGCCCCATTCGGTT	170208

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Query	3781	ATTTCTAAATTACGGTTCGGGTTTCGGTTCGGATCCTTGCGGATTCGGTTCGGGTTTCGGAT	3840
Sbjct	170207	ATTTCTAAATTACGGTTCGGGTTTCGGTTCGGATCCTTGCGGATTCGGTTCGGGTTTCGGAT	170148
Query	3841	AACCCGTTTAAATTATTTTCAAAATTTTAAAATTTTCATTATATATTTTAAACTTTTCGAA	3900
Sbjct	170147	AACCCGTTTAAATTATTTTCAAAATTTTAAAATTTTCATTATATATTTTAAACTTTTCGAA	170088
Query	3901	ATTTGTAAACAAAATAATATATTACATATAAAATTTCAATAATATGTGTCTGAAGTACCAAA	3960
Sbjct	170087	ATTTGTAAACAAAATAATATATTACATATAAAATTTCAATAATATGTGTCTGAAGTACCAAA	170028
Query	3961	ACTTAACATGTAAATTGGTTTGATTTGGATATTTGGATAGAAAATCAATCATATTTTATA	4020
Sbjct	170027	ACTTAACATGTAAATTGGTTTGATTTGGATATTTGGATAGAAAATCAATCATATTTTATA	169968
Query	4021	TATTTTTGGTGTTTTGAGTATGCTTTAACTATTTATACATGTACTTTTTAATGTTTTTAT	4080
Sbjct	169967	TATTTTTGGTGTTTTGAGTATGCTTTAACTATTTATACATGTACTTTTTAATGTTTTTAT	169908
Query	4081	ATATTTTCTAGTATTTTGAACAATTTAAAAGTATTATATATATTTTAGATGCTTTTTAAT	4140
Sbjct	169907	ATATTTTCTAGTATTTTGAACAATTTAAAAGTATTATATATATTTTAGATGCTTTTTAAT	169848
Query	4141	ATATATTCAATCTAAAAATAGTTAAATATATATGTATATTAATCTATTTTCGGATACATTC	4200
Sbjct	169847	ATATATTCAATCTAAAAATAGTTAAATATATATGTATATTAATCTATTTTCGGATACATTC	169788
Query	4201	GGATATCCAAAATATTTTGGTTCGGATCGGGTTCGGTTTTGGTTCTTTAAATACCAAAAA	4260
Sbjct	169787	GGATATCCAAAATATTTTGGTTCGGATCGGGTTCGGTTTTGGTTCTTTAAATACCAAAAA	169728
Query	4261	TTTAAACCTATTTCGGATATTCAATTAATTTTCGGTTCGGATTTGGTATTACTTTTGCAGAT	4320
Sbjct	169727	TTTAAACCTATTTCGGATATTCAATTAATTTTCGGTTCGGATTTGGTATTACTTTTGCAGAT	169668
Query	4321	CGGATTTCGGTTCGGTTCTTTGGATTTCAGTTTTTTTTGTCCAGCCCTACTCTGAACAGTAGA	4380
Sbjct	169667	CGGATTTCGGTTCGGTTCTTTGGATTTCAGTTTTTTTTGTCCAGCCCTACTCTGAACAGTAGA	169608
Query	4381	TAAAAAATAGAACCCTAAATTAATAGGTTAGATTTTGGTTAGGTCTTTCTAATTAGTATG	4440
Sbjct	169607	TAAAAAATAGAACCCTAAATTAATAGGTTAGATTTTGGTTAGGTCTTTCTAATTAGTATG	169548
Query	4441	GAGATTCTCGATTCTCTTCATTGCAGTGTGGTATGTCCAACCTCATTGTTTATGTACATA	4500
Sbjct	169547	GAGATTCTCGATTCTCTTCATTGCAGTGTGGTATGTCCAACCTCATTGTTTATGTACATA	169488
Query	4501	TCCAATTTAGTTTTGAGTCAAATGTTTAGTTACTTAAAGAGTTGAATGAAATAGGGGATGA	4560
Sbjct	169487	TCCAATTTAGTTTTGAGTCAAATGTTTAGTTACTTAAAGAGTTGAATGAAATAGGGGATGA	169428

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Query	4561	TATTGATGGCCAAGGTTCTCCCAAAGTAAAT-AACTTTGTTTATATTTTAAGTTAGCTTA	4619
Sbjct	169427	TATTGATGGCCAAGGTTCTCCCAAAGTAAATAAACTTTGTTTATATTTTAAGTTAGCTTA	169368
Query	4620	TAACATCAATAAAAAATGTCATTAAGTGGTTCAATAAAAAATGTCATTAAGTGGTTCCTCTA	4679
Sbjct	169367	TAACATCAATAAAAAATGTCATTAAGTGGTTCAATAAAAAATGTCATTAAGTGGTTCCTCTA	169308
Query	4680	ATATAATTATTTAACACACCTGGCTGTTGATAAATTTTTATGATCGTTTAATAATTTTAG	4739
Sbjct	169307	ATATAATTATTTAACACACCTGGCTGTTGATAAATTTTTATGATCGTTTAATAATTTTAG	169248
Query	4740	AAGTGGATAGTCTGTAAATGGTCTTTGATTGGTCGTCTTGATTTTTAAAAGTGGACTAAA	4799
Sbjct	169247	AAGTGGATAGTCTGTAAATGGTCTTTGATTGGTCGTCTTGATTTTTAAAAGTGGACTAAA	169188
Query	4800	CAAGAAGGCTTAGTAATAAATACTGAACCGGAAGTCTACTGGTTTCAATAGCTCGGTTTA	4859
Sbjct	169187	CAAGAAGGCTTAGTAATAAATACTGAACCGGAAGTCTACTGGTTTCAATAGCTCGGTTTA	169128
Query	4860	TCAATTTCTCTCGGCTCTGGGTTTAGTGAATCATGTGGCCCTGTGGGTTTAAACAAGGAA	4919
Sbjct	169127	TCAATTTCTCTCGGCTCTGGGTTTAGTGAATCATGTGGCCCTGTGGGTTTAAACAAGGAA	169068
Query	4920	CTCAATCAATCAACTGGTGACAAATCTGAACCGGAAATTGTATAATTCAAAGTGAACCGG	4979
Sbjct	169067	CTCAATCAATCAACTGGTGACAAATCTGAACCGGAAATTGTATAATTCAAAGTGAACCGG	169008
Query	4980	TTCTTGTAAAACAAATGGAACCCGTTTGTACTTTATCTCTCGTTTATTTTCTCAGTCACG	5039
Sbjct	169007	TTCTTGTAAAACAAATGGAACCCGTTTGTACTTTATCTCTCGTTTATTTTCTCAGTCACG	168948
Query	5040	AGTTTTTTTTTAGAGATCGACGAAGAACAAAATTTAGGCGAAACAAAAATAAAATGTTGGC	5099
Sbjct	168947	AGTTTTTTTTTAGAGATCGACGAAGAACAAAATTTAGGCGAAACAAAAATAAAATGTTGGC	168888
Query	5100	TAGGGTTTGTGGATTCAAGTGTTCTTCTCTCTGCTGAGTCTGCGGCTAGATTGTTCTG	5159
Sbjct	168887	TAGGGTTTGTGGATTCAAGTGTTCTTCTCTCTGCTGAGTCTGCGGCTAGATTGTTCTG	168828
Query	5160	TACGAGATCGATTCTGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAAGCAGGTTT	5219
Sbjct	168827	TACGAGATCGATTCTGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAAGCAGGTTT	168768
Query	5220	TGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTAGAGGATGC	5279
Sbjct	168767	TGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTAGAGGATGC	168708
Query	5280	GATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTTGATTTCTG	5339
Sbjct	168707	GATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTTGATTTCTG	168648

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Query	5340	TAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCCGGATCTTGTGATTTCTCTCTATCA	5399
Sbjct	168647		
Sbjct	168647	TAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCCGGATCTTGTGATTTCTCTCTATCA	168588
Query	5400	GAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAATATTCTGATAAAATG	5459
Sbjct	168587		
Sbjct	168587	GAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAATATTCTGATAAAATG	168528
Query	5460	TTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATCACCAAGCT	5519
Sbjct	168527		
Sbjct	168527	TTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATCACCAAGCT	168468
Query	5520	TGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGA	5579
Sbjct	168467		
Sbjct	168467	TGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGA	168408
Query	5580	TAGGGTTTCTGAAGCCTTGGAATTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAA	5639
Sbjct	168407		
Sbjct	168407	TAGGGTTTCTGAAGCCTTGGAATTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAA	168348
Query	5640	TGTCGTAACCTTCACCACCTTGGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCTGAAGC	5699
Sbjct	168347		
Sbjct	168347	TGTCGTAACCTTCACCACCTTGGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCTGAAGC	168288
Query	5700	CGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGG	5759
Sbjct	168287		
Sbjct	168287	CGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGG	168228
Query	5760	AACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAG	5819
Sbjct	168227		
Sbjct	168227	AACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAG	168168
Query	5820	GAAGATGGAGGAGGTGAGCCACATCATAACCAATGTTGTAATCTATAGTGCAATCATTGA	5879
Sbjct	168167		
Sbjct	168167	GAAGATGGAGGAGGTGAGCCACATCATAACCAATGTTGTAATCTATAGTGCAATCATTGA	168108
Query	5880	TAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGA	5939
Sbjct	168107		
Sbjct	168107	TAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGA	168048
Query	5940	GAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTC	5999
Sbjct	168047		
Sbjct	168047	GAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTC	167988
Query	6000	TGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGCCC	6059
Sbjct	167987		
Sbjct	167987	TGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGCCC	167928
Query	6060	TGATGTTGTAACCTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTTGA	6119
Sbjct	167927		
Sbjct	167927	TGATGTTGTAACCTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTTGA	167868

Group 4

Query	6120	GGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACATA	6179
Sbjct	167867	GGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACATA	167808
Query	6180	TAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATGTT	6239
Sbjct	167807	TAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATGTT	167748
Query	6240	TTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATAGA	6299
Sbjct	167747	TTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATAGA	167688
Query	6300	CGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTCTCCATGAGATGACTGA	6359
Sbjct	167687	CGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTCTCCATGAGATGACTGA	167628
Query	6360	AACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTCACGGGTTCTATCTGGT	6419
Sbjct	167627	AACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTCACGGGTTCTATCTGGT	167568
Query	6420	GGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC	6479
Sbjct	167567	GGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC	167508
Query	6480	TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAACTAAAAGA	6539
Sbjct	167507	TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAACTAAAAGA	167448
Query	6540	TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC	6599
Sbjct	167447	TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC	167388
Query	6600	CTTCAATGGTGTGGAACCTGATGTTCAAACCTTACAATATATTGATCAGCGGCTTGATCAA	6659
Sbjct	167387	CTTCAATGGTGTGGAACCTGATGTTCAAACCTTACAATATATTGATCAGCGGCTTGATCAA	167328
Query	6660	TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT	6719
Sbjct	167327	TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT	167268
Query	6720	CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA	6779
Sbjct	167267	CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA	167208
Query	6780	TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCAAACGTAGTGAC	6839
Sbjct	167207	TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCAAACGTAGTGAC	167148
Query	6840	CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT	6899
Sbjct	167147	CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT	167088

Group 4

Query	6900	TTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT	6959
Sbjct	167087	TTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT	167028
Query	6960	TTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGAT	7019
Sbjct	167027	TTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGAT	166968
Query	7020	TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG	7079
Sbjct	166967	TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG	166908
Query	7080	TAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATGAGTATGGTATG	7139
Sbjct	166907	TAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATGAGTATGGTATG	166848
Query	7140	TAAGTTTCTGTTTCAGTCTATGTATTTTTTATATAAACAAGAATGTATACATTCTTTTGTG	7199
Sbjct	166847	TAAGTTTCTGTTTCAGTCTATGTATTTTTTATATAAACAAGAATGTATACATTCTTTTGTG	166788
Query	7200	TGTAGCTTCAGATTGATGATACACGTTCTGGAATTAACCATTGGTTTGGTTTGCATTGT	7259
Sbjct	166787	TGTAGCTTCAGATTGATGATACACGTTCTGGAATTAACCATTGGTTTGGTTTGCATTGT	166728
Query	7260	AGGATCTATCATTTGGGGGATGAATGATCAAAGATTTTCTTCTGTTTGCGCAGCAGAGCT	7319
Sbjct	166727	AGGATCTATCATTTGGGGGATGAATGATCAAAGATTTTCTTCTGTTTGCGCAGCAGAGCT	166668
Query	7320	TCAATGTCATTTTGTTTCTGCTGCTGCATGTATACCCTACTAATGTTTGATCAAATCGTT	7379
Sbjct	166667	TCAATGTCATTTTGTTTCTGCTGCTGCATGTATACCCTACTAATGTTTGATCAAATCGTT	166608
Query	7380	GAATAGAGTGATCATAGTGAAAAATTGTGTGGTTAGTAAGTTATTTTGCTGCTATTCTAA	7439
Sbjct	166607	GAATAGAGTGATCATAGTGAAAAATTGTGTGGTTAGTAAGTTATTTTGCTGCTATTCTAA	166548
Query	7440	TGACAGCCTTTTATGCGTCTATTGTCTGGGCTTAATAAATTTGACCATTTCCAATTAAAT	7499
Sbjct	166547	TGACAGCCTTTTATGCGTCTATTGTCTGGGCTTAATAAATTTGACCATTTCCAATTAAAT	166488
Query	7500	TCCATACACTTGTTTCACGCAAGATTATTGGTCTGAACTAAAGAGGCACACCTTCCAGAA	7559
Sbjct	166487	TCCATACACTTGTTTCACGCAAGATTATTGGTCTGAACTAAAGAGGCACACCTTCCAGAA	166428
Query	7560	GATTTTCAGGTGTTAAAGATGTTTAGGTGTCTGCCCGTTCTGTAGCTGTCACCATGGTTA	7619
Sbjct	166427	GATTTTCAGGTGTTAAAGATGTTTAGGTGTCTGCCCGTTCTGTAGCTGTCACCATGGTTA	166368
Query	7620	TCGTCAAGCTCGGTCTTCATGAGAGCTGATAGCTGTGATGCCATCTTCCTCCTCTTCTTC	7679
Sbjct	166367	TCGTCAAGCTCGGTCTTCATGAGAGCTGATAGCTGTGATGCCATCTTCCTCCTCTTCTTC	166308

Group 4

Query	7680	ATATTGGCTCTGTCCTGCCTTGTCTGCTCCCATGTGGGTTTCAGGAGGAGATCATGTTCTT	7739
Sbjct	166307	ATATTGGCTCTGTCCTGCCTTGTCTGCTCCCATGTGGGTTTCAGGAGGAGATCATGTTCTT	166248
Query	7740	TTAATCTTGGTGGAAATGTTGTTGTGCTTATGCTTCTCTGGTTCGCCTCTTGA	7799
Sbjct	166247	TTAATCTTGGTGGAAATGTTGTTGTGCTTATGCTTCTCTGGTTCGCCTCTTGA	166188
Query	7800	TAGCTTCATTCTTTATCTCCAAATTGCTATGAAATCAATTTACCATAAGTAGAATAAACT	7859
Sbjct	166187	TAGCTTCATTCTTTATCTCCAAATTGCTATGAAATCAATTTACCATACGTAGAATAAACT	166128
Query	7860	TGCAGATTCACTTCTATTATTGCTTAAGCTTTTGTTAATCAACAAAGAAACCAGAGACGAG	7919
Sbjct	166127	TGCAGATTCACTTCTATTATTGCTTAAGCTTTTGTTAATCAACAAAGAAACCAGAGACGAG	166068
Query	7920	AAATACAAACTCTATAAGCTTCTCTTTTTTCTTTCTTGATAGTAAAACCGGTTAGAGAGT	7979
Sbjct	166067	AAATACAAACTCTATAAGCTTCTCTTTTTTCTTTCTTGATAGTAAAACCGGTTAGAGAGT	166008
Query	7980	AGAGATTGATCATATGAACTAAAAATCGATACTAAAACGGTTTGGCTCCGACTTATAAAC	8039
Sbjct	166007	AGAGATTGATCATATGAACTAAAAATCGATACTAAAACGGTTTGGCTCCGACTTATAAAC	165948
Query	8040	CGGAACCCACCGTTTTGCATCTCTCTCTCAAACATCACACAATGTCCAAGATGAAGAAG	8099
Sbjct	165947	CGGAACCCACCGTTTTGCATCTCTCTCTCAAACATCACACAATGTCCAAGATGAAGAAG	165888
Query	8100	TATTTGTGTTGTCATCTCTCTGGGTGAGGAGATGCAAATGTTATATTCTAATTGTTTTCA	8159
Sbjct	165887	TATTTGTGTTGTCATCTCTCTGGGTGAGGAGATGCAAATGTTATATTCTAATTGTTTTCA	165828
Query	8160	GTGCTTGGTCTAACTTTTTTAAGAGATTACTCCAGTGGTTGGATCAAAGAAAGAGTCAA	8219
Sbjct	165827	GTGCTTGGTCTAACTTTTTTAAGAGATTACTCCAGTGGTTGGATCAAAGAAAGAGTCAA	165768
Query	8220	CATTGCATTGTGTAAGGTGACGAAAACAGTTAAAGTAAGTGAGAACAATACTTCAATG	8279
Sbjct	165767	CATTGCATTGTGTAAGGTGACGAAAACAGTTAAAGTAAGTGAGAACAATACTTCAATG	165708
Query	8280	CTTTTCTTGTGACAACCTGTGTAATCATCGCATTTGAATATATATGTATATGATGCTTAT	8339
Sbjct	165707	CTTTTCTTGTGACAACCTGTGTAATCATCGCATTTGAATATATATGTATATGATGCTTAT	165648
Query	8340	GATGAAGCTATGAGAATAGGCAAATAGGGTCTGTGTTATTTCCCTGCGATTCTAGATTCT	8399
Sbjct	165647	GATGAAGCTATGAGAATAGGCAAATAGGGTCTGTGTTATTTCCCTGCGATTCTAGATTCT	165588
Query	8400	GATTTGTTTTTCCTTCTTAATATTTAGATTAGGTGGTCTTGCTTATCCTGTTTTAGTATT	8459
Sbjct	165587	GATTTGTTTTTCCTTCTTAATATTTAGATTAGGTGGTCTTGCTTATCCTGTTTTAGTATT	165528

Group 4

Query	8460	AGAGTCGGAGTTTTGGGGATGAATCATCCCGGATGATATATACAATTGTGTATTTTATGA	8519
Sbjct	165527	AGAGTCGGAGTTTTGGGGATGAATCATCCCGGATGATATATACAATTGTGTATTTTATGA	165468
Query	8520	ATTTTCAGTTTTTAGTGGATAATGAACACGTTAAC	8553
Sbjct	165467	ATTTTCAGTTTTTAGTGGATAATGAACACGTTAAC	165434

Score = 2963 bits (1541), Expect = 0.0
 Identities = 1885/2052 (91%), Gaps = 18/2052 (0%)
 Strand=Plus/Minus

Query	5090	AAATGTTGGCTAGGGTTTGTGGATTCAAGTGTCTTCTTCTCTGCTGAGTCTGCGGCTA	5149
Sbjct	161145	AAATGTTGGCTAGGGTTTGCAGATTCGAGTCTTCTCTTCTGCTGAGTCTGCGGCTA	161086
Query	5150	GATTGTTCTGTACGAGATCGATTTCGTGATACTCTGGCCAAGGCAAGC-----GGAGAGA	5203
Sbjct	161085	GATTTTTCTGTACGGGATCGATTTCGTGATGCTCTGGCCGAGAAAAGCAGGGATGGAGAGA	161026
Query	5204	GTTGCGAAGCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCA	5263
Sbjct	161025	GTGGCGAAGCAGGTTTTAGAGGAGAGAGTTTGAAGCTGCAAAGTGGATCTTATGAAATCA	160966
Query	5264	AAGGTTTAGAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTT	5323
Sbjct	160965	AAGGTTTAGAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTT	160906
Query	5324	CTGTGGTTGATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCCGGATCTTG	5383
Sbjct	160905	CTGTGATTGATTTCAACAAGCTAATGGGTGCGGTGGTGAGAATGGAACGCCCCGGATCTTG	160846
Query	5384	TGATTTCTCTCTATCAGAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCA	5443
Sbjct	160845	TGATTTCTCTCTATCAAAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCA	160786
Query	5444	ATATTCTGATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCCTTTGCTTTGTCTACATTTG	5503
Sbjct	160785	CCATTCTGATAAAATGTTTCTGCAGTTGCTCTAAGCTCCCCCTTTGCTTTGTCTACATTTG	160726
Query	5504	GTAAGATCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATG	5563
Sbjct	160725	GTAAGCTCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCACG	160666
Query	5564	GATTATGTGTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAA	5623
Sbjct	160665	GATTATGTCTTGATCACAGGGTTTCTGAAGCCTTGGATTTGTTTCATCAAATTT-----	160612
Query	5624	CGACATGTAGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGG	5683
Sbjct	160611	-----GTAGACCAGATGTCCTAACGTTTCACCACGCTGATGAATGGTCTTTGCCGCGAGG	160558

Group 4

Query	5684	GTAGAATTGTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTA	5743
Sbjct	160557	GTCGAGTTGTCGAAGCCGTAGCTCTGCTTGATCGGATGGTGGAAAATGGTCTCCAGCCTG	160498
Query	5744	CCCAGATTACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTG	5803
Sbjct	160497	ACCAGATTACTTACGGAACATTTGTAGATGGGATGTGTAAGATGGGCGACACTGTGTCTG	160438
Query	5804	CACTGAATCTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATAACCAATGTTGTAATCT	5863
Sbjct	160437	CATTGAATCTTCTGAGGAAGATGGAGGAGATAAGCCACATCAAACCAATGTGGTTATCT	160378
Query	5864	ATAGTGCAATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTT	5923
Sbjct	160377	ATAGTGCCATCATTGATGGCCTTTGTAAAGATGGACGCCATAGCGATTCTCATAATCTTT	160318
Query	5924	TCACTGAAATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAG	5983
Sbjct	160317	TCATTGAAATGCAAGACAAGGGAATCTTTCCAAATATAGTTACCTACAACGTATGATCG	160258
Query	5984	TTGGTTTTTTGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAG	6043
Sbjct	160257	GTGGATTTTGCATCTCTGGTAGATGGAGTGCAGCCAGCGGTTGTTGCAAGAAATGTTAG	160198
Query	6044	AAAGGAAGATCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGG	6103
Sbjct	160197	AAAGGAAGATCAGCCCTAATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGG	160138
Query	6104	AAGGCAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCC	6163
Sbjct	160137	AAGGCAAGTTCTTCGAGGCTGCAGAATTATACGATGAGATGCTTCCAAGGGGTATCATTC	160078
Query	6164	CTAATACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATG	6223
Sbjct	160077	CTAATACAATCACATATAATTCAATGATCGATGGGTTTTGCAAACAGGATCGTCTTGATG	160018
Query	6224	CTGCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTT	6283
Sbjct	160017	CTGCTGAGGACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGGACGTATTCACTT	159958
Query	6284	TCAATACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTC	6343
Sbjct	159957	TCATACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTC	159898
Query	6344	TCCATGAGATGACTGAAACAGGATTAGTTGCTGACACAACACTACTTACAACACTCTTATTC	6403
Sbjct	159897	TCCATGAGATGCCTAGAAGAGGATTAGTTGCTAACACAGTTACTTACAACACTCTTATTC	159838
Query	6404	ACGGGTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCT	6463
Sbjct	159837	ACGGGTTCTGTCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAGCAGATGATTT	159778

Group 4

Query	6464	CTAGTGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATA	6523
Sbjct	159777	CTAGTGGTGTGTGCCCTGATATCGTTACTTGTAACTTTGCTGGACGGTCTCTGCGATA	159718
Query	6524	ATGGGAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATC	6583
Sbjct	159717	ATGGGAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTAAGATGGATC	159658
Query	6584	TTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTACAATATATTGA	6643
Sbjct	159657	TTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCTAACTTACAATATATTGA	159598
Query	6644	TCAGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGC	6703
Sbjct	159597	TCTGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGC	159538
Query	6704	CCCACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCA	6763
Sbjct	159537	CACACAGAGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGACTATGCA	159478
Query	6764	AGCAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCT	6823
Sbjct	159477	AGCAGAGCCGCCTAGATGAGGCTACACAAATGTTTGTTTCGATGGGTAGCAAGAGCTTCT	159418
Query	6824	CTCCAAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTG	6883
Sbjct	159417	CTCCAAACGTAGTGACATTTAACACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTG	159358
Query	6884	ATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTA	6943
Sbjct	159357	ATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTGATGCAATTA	159298
Query	6944	CTTACATCACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACA	7003
Sbjct	159297	TTTACATCACTTTGATTTATGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACA	159238
Query	7004	TTTTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGC	7063
Sbjct	159237	TTTTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGC	159178
Query	7064	TGACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGC	7123
Sbjct	159177	TGACTGGTTTTTGGAGTAAAGAGGAACTAGAAAGGGCAGTGGCAATGCTTGAGGATCTGC	159118
Query	7124	AGATGAGTATGG	7135
Sbjct	159117	AGATGAGTGTGG	159106

Score = 2807 bits (1460), Expect = 0.0
 Identities = 1966/2199 (89%), Gaps = 56/2199 (2%)
 Strand=Plus/Minus

Group 4

Query	5720	TGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGGAACAATCGTAGATGGGATGT	5779
Sbjct	177048	TGCTAGAAGATGGTCTCCAGCCTAACCAGATTACTTATGGAACAATCGTGGATGGGATGT	176989
Query	5780	GTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAGGAAGATGGAGGAGGTGAGCC	5839
Sbjct	176988	GTAAGATGGGAGACACTGTGTCTGCATTGAATCTTCTGAGGAAGATGGAGGAGGTGAGCC	176929
Query	5840	ACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGATAGCCTTTGTAAAGACGGAC	5899
Sbjct	176928	ACATCAAACCCAATGTGGTAATCTG-----GCCTTTGGAAAGACGGAC	176886
Query	5900	GTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGAGAAAGGAATCTTTCCCGATT	5959
Sbjct	176885	GTCATACCGATGCTCAAAATCTTTTCACTGAAATGCAAGACAAGGGAATCTTTCCCAATT	176826
Query	5960	TATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGG	6019
Sbjct	176825	TATTTACCTACAGCTGTATGATTAATGGATTTTGTAGCTCTGGTAGATGGAGTGAAGCCC	176766
Query	6020	AGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGA---TCAGCCCTGATGTTGTAACCTATA	6076
Sbjct	176765	AGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGAAGATCAGCCCTGATGTTGTAACCTATA	176706
Query	6077	ATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTTGAGGCTGAAGAATTATACG	6136
Sbjct	176705	ATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAATTCTTTGAGGCTGAAGAATTATACG	176646
Query	6137	ATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACATATAGTTCAATGATCGATG	6196
Sbjct	176645	ATGAGATGCTTCCAAGGGGTATAATCCCTAGTACAATCACATATAGTTCAATGATCGATG	176586
Query	6197	GATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATGTTTTATTTGATGGCTACCA	6256
Sbjct	176585	GATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATGTTTTATTTGATGGCTACCA	176526
Query	6257	AGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATAGACGGATATTGTGGGGCTA	6316
Sbjct	176525	AGGGCTGCTCTCCGGACATAATCACTTTCAATACTCTCATAGCCGGATACTGTAGAGCTA	176466
Query	6317	AGAGGATAGATGATGGAATGGAACCTTCTCCATGAGATGACTGAAACAGGATTAGTTGCTG	6376
Sbjct	176465	AGAGGGTAGATGATGGAATAAACTTCTCCATGAGATGACTGAAGCAGGATTAGTTGCTA	176406
Query	6377	ACACAACACTTACAACACTCTTATTACGGGTTCTATCTGGTGGGCGATCTTAATGCTG	6436
Sbjct	176405	ACACAATTACTTACACCACTCTTATTACGGGTTCTGTGAGGTGGGCGATCTTAATGCTG	176346
Query	6437	CTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTTGTGCCCTGATATCGTTACTTG TG	6496
Sbjct	176345	CTCAAGACCTTCTACAGGAGATGGTCTCTAGTGGTGTGTGCCCTAATGTCGTTACTTGTA	176286

Group 4

Query	6497	ACACTTTGCTGGATGGTCTCTGCGATAATGGGAACTAAAAGATGCATTGGAAATGTTTA	6556
Sbjct	176285	ACACTTTGCTGGACGGTCTCTGCGATAATGGGAACTAAAAGATGCATTGGAAATGTTTA	176226
Query	6557	AGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCCCTTCAATGGTGTGGAAC	6616
Sbjct	176225	AGGCTATGCAGAAGAGTAAGATGGATATTGATGCTAGTCACCCCTTTAATGGTGTGGAAC	176166
Query	6617	CTGATGTTCAAACCTTACAATATATTGATCAGCGGCTTGATCAATGAAGGGAAGTTTTTAG	6676
Sbjct	176165	CTGATGTTCAAACCTTACAATATATTGATCAGTGGCTTGATCAATGAAGGGAAGTTTTTAG	176106
Query	6677	AGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGTCCCAGATACTATCACCT	6736
Sbjct	176105	AGGCCGAGGAATTATACGAGGAGATGCCACACAGAGGTATAGTCCCAGATACTATCACCT	176046
Query	6737	ATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCTAGATGAGGCTACACAAATGT	6796
Sbjct	176045	ATAACTCAGTGATCCATGGTTTATGCAAGCAAAGCCGCTAGATGAGGCTACACAAATGT	175986
Query	6797	TTGATTTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGACCTTTACTACACTCATT	6856
Sbjct	175985	TTGATTTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGACCTTTACTACACTCATT	175926
Query	6857	ATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTC	6916
Sbjct	175925	ATGGATACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTC	175866
Query	6917	GAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGATTTGTGGTTTTTCGTAAAG	6976
Sbjct	175865	GAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGATTCATGGTTTTTCGTAAAG	175806
Query	6977	TGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTATC	7036
Sbjct	175805	TGGGTAATATTAATGGGGCTCTAGATATTTTCCAGGAGATGATGGCAAGTGGTGTGTATC	175746
Query	7037	CTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAA	7096
Sbjct	175745	CTGATACCATTACTATCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAA	175686
Query	7097	GGGCAGTGGCAATGCTTGAGAACTGCAGATGAGTATGG	7135
Sbjct	175685	GGGCAGTGGCAATGCTTGAGGATCTGCAGATGAGTGTGG	175647

Score = 1698 bits (883), Expect = 0.0
 Identities = 1091/1170 (93%), Gaps = 13/1170 (1%)
 Strand=Plus/Plus

Query	6420	GGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC	6479
Sbjct	574	GGGCGATCTTAATTCTGCTCAAGACCTTTTACAGGAGATGATTTCTAGTGGTGTGTGCCC	633

Group 4

Query	7259	TAGGATCTATCATTTTGG-GGGATGAATGATCAAAGA-TTTTCTTCTGTTTGCGCAGCAGA	7316
Sbjct	1414	TAGGATC-ATCATTTGGTGGGGTGAATGATCAAAGATTTTCTACTCTTT--GCAGCAGA	1470
Query	7317	GCTTCAATGTCATTTTGTCTGCTGCTGCATGTATACCCTACTAATGTTTGATCAAATC	7376
Sbjct	1471	GCTTCAATG-CATTTTGTCTGCTGCTGCATTTGTACCCTACTAATGTTTGATCAAATC	1529
Query	7377	GTTGAATAGAGTGATCATAGTG-AAAAATTGTGTGGTTAGTAAGTTATTTTGCTGCTATT	7435
Sbjct	1530	GTGGAATAGAGTGATCATAGTGTAATAAATTGTGTGGTCAATGAGCTGTTTGCTGCTATT	1589
Query	7436	CTAATGACAGCCTTTTATGCGTCTATTGTCTGGGCTTAATAAATTTGACCATTTCCAATT	7495
Sbjct	1590	CTAATGACAGCC-TTTATGCGTCTATTGT---AGTTTAATAAATTTGACCATTTCCAATT	1645
Query	7496	AAATTCCATACACTTGTTCACGCAAGATTATTGGTCTGAACTAAAGAGGCACACCTTCC	7555
Sbjct	1646	AAGTTCCATACACTTG-TTCACGCAAGATTATTGGTGCGAATAAAGAAGCACACCTTCC	1704
Query	7556	AGAAGATTTTCAGGTGTTAAAGATGTTTAG	7585
Sbjct	1705	AGAAGACTTCAGGTGTTAAAGATGTTTAG	1734

Score = 687 bits (357), Expect = 0.0
 Identities = 502/572 (87%), Gaps = 12/572 (2%)
 Strand=Plus/Plus

Query	5537	TTGTTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGATAGGGTTTCTGAAGCCT	5596
Sbjct	18	TTGTTACCTTCAACACCCTTCTCCACGATTATGTGTGGAAGATAGGGTTTCTGAAGCCT	77
Query	5597	TGGATTTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAATGTCGTAACCTTCACCA	5656
Sbjct	78	TGGATTTGTTTCATCAAATGTGTAAA-----CCAAATGTCGTAACCTTCACCA	125
Query	5657	CTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTGCGAAGCCGTAGCTCTGCTTGATC	5716
Sbjct	126	CGCTGATGAACGGTCTTTGCCGCGAGGGTAGAGTTGTGCGAGGCCGTAGCTCTGCTTGATC	185
Query	5717	GGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGGAACAATCGTAGATGGGA	5776
Sbjct	186	GGATGGTAGAAGATGGTCTCCAGCCTAACCAGATTACTTACGGAACAATTGTAGATGGGA	245
Query	5777	TGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAGGAAGATGGAGGAGGTGA	5836
Sbjct	246	TGTGTAAGATGGGAGACACTGTGTCTGCATTGAATCTTCTGAGGAAGATGGAGGAGTTGA	305
Query	5837	GCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGATAGCCTTTGTAAAGACG	5896
Sbjct	306	GCCACATCAAACCGGATGTGGTAATCTATAGTGCCATCATTGATGGCCTTTGGAAAGACG	365

Group 4

Query	5897	GACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGAGAAAGGAATCTTTCCCG	5956
Sbjct	366	GACGTCATACCGATGCTCAAAATCTTTTCATTGAAATGCAAGACAAGGAATCTTTCCAG	425
Query	5957	ATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTCTGGTAGATGGAGCGACG	6016
Sbjct	426	ATATAGTTACCTACAGCTGTATGATTAATGGATTTTGTAGCTCTGGTAAATGGAGTGAAG	485
Query	6017	CGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGCCCTGATGTTGTAACCTATA	6076
Sbjct	486	CCCAGCGCTTGTTGCAAGAAATGTTAGTAAGGAAGATCAGCCCTGATGTTGTAACCTTTCA	545
Query	6077	ATGCTTTGATCAATGCATTTGTCAAGGAAGGC	6108
Sbjct	546	GTGGATTGATCAATGCATTGGTCAAAGAGGGC	577

Score = 164 bits (85), Expect = 8e-36
 Identities = 128/147 (87%), Gaps = 3/147 (2%)
 Strand=Plus/Plus

Query	7668	CTCCTCTTCTTCATATTGGCTCTGTCCTGCCTTGTCTGCTCCCATGTGGGTTTCAGGAGGA	7727
Sbjct	2657	CTCCTCTTCTTCATATTGGTTCGGTCCGTCTGCCTTGTCTGCTCCCATGTGGGTTAAGGAGGA	2716
Query	7728	GATCATGTTCTTTTAATCTTGGTGGAAATGTTGTTGTCGCTTATGCTTCTCTGGTTTCG--	7785
Sbjct	2717	GATCATGTTTTTAAGATCGTGGTGGAAATGTTGGTGTGGTTGTCCTTCGCTGATTTCGCC	2776
Query	7786	-CCTCTTGACTTGCTTAGCTTCATTCT	7811
Sbjct	2777	TCCTCTTGATTTGCTTAGCTTCATTCT	2803

Score = 150 bits (78), Expect = 9e-32
 Identities = 316/435 (72%), Gaps = 0/435 (0%)
 Strand=Plus/Plus

Query	6058	CCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTT	6117
Sbjct	770	CCTGATGTTCAAACCTTACAATATATTGATCAGCGGATTGATTAATGAAGGGAAGTTTTTA	829
Query	6118	GAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACA	6177
Sbjct	830	GAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGTCCCAGATACTGTTACC	889
Query	6178	TATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATG	6237
Sbjct	890	TATAGCTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGATGAGGCTACACAAATG	949

Group 4

```

Query 6238 TTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATA 6297
      ||| ||| ||||| || ||||| ||| ||||| ||| ||| ||| ||| |||||
Sbjct 950 TTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGACATTTAACACACTCATT 1009

Query 6298 GACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTCTCCATGAGATGACT 6357
      || ||| ||| ||| ||| ||| ||||| ||| ||||| ||| ||| ||||| ||
Sbjct 1010 ACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCTTTTCTGCGAGATGGGT 1069

Query 6358 GAAACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTCACGGGTTCTATCTG 6417
      || ||| ||||| ||| ||| ||||| ||| ||||| ||| ||| ||| |||
Sbjct 1070 CGAAGAGGGATAGTTGCTAATGCAATTACTTACATCACTTTGATTCGTGGTTTTTCGTAAA 1129

Query 6418 GTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGC 6477
      ||||| || ||||| ||||| ||||| ||| ||| ||||| ||| ||||| |||
Sbjct 1130 GTGGGTAATATTAATGGGTCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTAT 1189

Query 6478 CCTGATATCGTTACT 6492
      ||||| || |||||
Sbjct 1190 CCTGATACCATTACT 1204

```

Score = 144 bits (75), Expect = 5e-30
 Identities = 180/225 (80%), Gaps = 3/225 (1%)
 Strand=Plus/Plus

```

Query 1099 ACCCCTAGAGTAAACCTTAAGGTTTACC-AACCAATAGAAATCACTCATTTCACAGTTGA 1157
      ||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||| |||
Sbjct 172146 ACCCCTAGAGTGAACATTTAGGTTTACCCCAACCAATAGGAATCAAGTATTTTATAATTAA 172205

Query 1158 TATCTTTTA-AAAAAGTAAACAAAATATTGTGCGAGTTATATTACATTTTTTAAAATAAAAA 1216
      ||| |||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct 172206 TATTTTTTTTTTAAAAAGAAAAGAAAATATTGTCAAGTTATATTATGTTTTTAAAATAAATA 172265

Query 1217 TATTAAAAAATAAAAAATAATAATATATGCAAAAAAAGATTTTTTAAAAGATTTTAAAT 1276
      | || |||| ||||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Sbjct 172266 AAATATAAAAAAATAATAATAGCCGTTACAAAAAATGAATTTTTGAAAACATTTTTTAAAT 172325

Query 1277 TTCGTCAACAAACACTAAACTCTAAACTCTAAATCCTAAACCT 1321
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 172326 ATCGTCAA-AAAACACTAAACCTTAAACCTTAAATCCTAAACCT 172369

```

Score = 144 bits (75), Expect = 5e-30
 Identities = 180/225 (80%), Gaps = 3/225 (1%)
 Strand=Plus/Plus

```

Query 1619 AGGGTTTAGGATTTAGGGTTTAAAGGTTTAGTGTTTT-TTGACGATATTAAAAATAGTTTT 1677
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 172667 AGGGTTTAGGATTTAGAGTTTAGAGTTTAGTGTTTTGTTGACGAAATTAAAATCTTTTTA 172726

```

Group 4

```

Query 1678      CAAAAATTCATTTTTGTACGGCTATTATTTTTTTTTTATATTTATTTATTTTAAAAA 1737
               |||| | |||||| | |||||||| ||| | | |||||||||
Sbjct 172727    AAAAATCTTTTTTTTGCATATATTATTATTTTATTTTAAATATTTTATTTTAAAAA 172786

Query 1738      CATAATATAACTTGACAATATTTTCTTTTCTTTTAAAAAAATATTAATTATGAAATAC 1797
               |||||||| |||||||| || ||||| ||| ||| | |||||
Sbjct 172787    TGTAATATAACTCGACAATATTTGTTTACTTTTT-TAAAAGATATCAACTGTGAAATGA 172845

Query 1798      TTGATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTAGGGGT 1842
               |||| |||||||| || || |||||
Sbjct 172846    GTGATTTCTATTGGTT-GGTGAACCTTAAGGTTTACTCTAGGGGT 172889

```

Score = 141 bits (73), Expect = 7e-29
 Identities = 107/119 (89%), Gaps = 3/119 (2%)
 Strand=Plus/Minus

```

Query 2918      AAAGAATGAAAGACATTTTTCTTTTCCAAATT-ACAATCCCTAGATAATTTTATTTTGTA 2976
               ||||||||| ||||||||| |||| || | |||||||||
Sbjct 158952    AAAGAATGAAAGACACTTTTCTTTTCCAAATTTACAAGGCCTTGTTGATTTTATTTTGTA 158893

Query 2977      GGTGCATTCCATCGGTTATGATTACAGAATAGCTACGCTTCTCTATTGATTCTTATTGC 3035
               |||| ||||||||| || |||||||||
Sbjct 158892    GGTGAATTCCATCGGTTATGATTATTG--TAGCTACGCTTCTCTATTGATTCTTATTGC 158836

```

Score = 89.1 bits (46), Expect = 3e-13
 Identities = 54/58 (93%), Gaps = 0/58 (0%)
 Strand=Plus/Minus

```

Query 1519      AGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG 1576
               ||||||| |||| |||| |||||||||
Sbjct 4367      AGGGTTTAGTATTTAGAATTTAAGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG 4310

```

Score = 87.2 bits (45), Expect = 1e-12
 Identities = 68/77 (88%), Gaps = 2/77 (2%)
 Strand=Plus/Minus

```

Query 4413      TTTTGGTTAGGTCTTTCTAATTAGTATGGAGATTCTCGATTCTTCTCATTGCAG--TGT 4470
               ||||||||| ||||||||| || | ||||||||| |||
Sbjct 158483    TTTTGGTTAGGTCTTGCTAATTAGTATGGAGTTGCCTTATTCCTTCTCATTGCAGTGTGT 158424

Query 4471      GGTATGTCCAACATCATT 4487
               |||||||| |||||
Sbjct 158423    GGTATGTCCTACTCATT 158407

```

Group 4

Score = 85.3 bits (44), Expect = 5e-12
 Identities = 56/62 (90%), Gaps = 0/62 (0%)
 Strand=Plus/Plus

```
Query 1515 CCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTT 1574
          |||||
Sbjct 4686 CCCAAGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTAGGGTTTAGGGTTT 4745

Query 1575 AG 1576
          ||
Sbjct 4746 AG 4747
```

Score = 83.4 bits (43), Expect = 2e-11
 Identities = 62/69 (89%), Gaps = 1/69 (1%)
 Strand=Plus/Plus

```
Query 1586 TTATCCAAGGGTTTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAAGGTT 1645
          ||| |||||
Sbjct 88893 TTACCCAAAGGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGA-TTAGAGTTTAGGGTT 88951

Query 1646 TAGTGTTTT 1654
          |||| ||||
Sbjct 88952 TAGTATTTT 88960
```

Score = 83.4 bits (43), Expect = 2e-11
 Identities = 53/58 (91%), Gaps = 0/58 (0%)
 Strand=Plus/Minus

```
Query 3153 TTCTGTGATTTTCATCAAGTTTTTTGAGAACAGAAGAAGCAAAAAAGAAAACGAGCAGAG 3210
          |||||
Sbjct 158794 TTCTGTGATTTTCATCAAATTTTTTAAAAACAGAAAAAGCAAAGAAGAAAACGAGCAGAG 158737
```

Score = 81.4 bits (42), Expect = 7e-11
 Identities = 61/68 (89%), Gaps = 1/68 (1%)
 Strand=Plus/Plus

```
Query 1493 TTATCCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTT 1552
          ||| |||||
Sbjct 88893 TTACCCAAAGGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGA-TTAGAGTTTAGGGTT 88951

Query 1553 TAGAATTT 1560
          ||| ||||
Sbjct 88952 TAGTATTT 88959
```

Group 4

Score = 73.7 bits (38), Expect = 1e-08
Identities = 70/86 (81%), Gaps = 0/86 (0%)
Strand=Plus/Minus

```
Query 1497 CCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGA 1556
          ||||| ||| | | ||| ||||| ||||| ||||| ||||| |||||
Sbjct 4396 CCAAGGGTTCAGGCTTTTTCCTAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGG 4337

Query 1557 ATTTAGGGTTTAGGGTTTAGAGTTTA 1582
          ||||| ||||| ||||| |||||
Sbjct 4336 GTTTAGAATTTAGGGTTTAGGGTTTA 4311
```

Score = 71.8 bits (37), Expect = 5e-08
Identities = 73/86 (84%), Gaps = 2/86 (2%)
Strand=Plus/Plus

```
Query 1496 TCCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAG 1555
          ||||| ||| || ||| || ||||| ||||| ||||| || ||||| |||||
Sbjct 88985 TCCAAGGGTTTATGGTTTATCCAAGGGTTTAAGGTTTATGA-TTAGAGTTTAGGGTTTAG 89043

Query 1556 AATTTAGGGTTTAGGGTTTAGAGTTT 1581
          | |||| ||||| ||||| |||||
Sbjct 89044 TA-TTAGAGTTTAGGGTTTAGTGTTT 89068
```

Score = 68.0 bits (35), Expect = 7e-07
Identities = 39/41 (95%), Gaps = 0/41 (0%)
Strand=Plus/Plus

```
Query 7600 TGTAGCTGTCAACCATGGTTATCGTCAAGCTCGGTCTTCATG 7640
          ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 2557 TGTAGCTGTCTCCATGGTTATCATCAAGCTCGGTCTTCATG 2597
```

Score = 68.0 bits (35), Expect = 7e-07
Identities = 43/47 (91%), Gaps = 0/47 (0%)
Strand=Plus/Minus

```
Query 1614 GGTTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTTTTGACG 1660
          ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4344 GGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGTATTTCTGACG 4298
```

Score = 68.0 bits (35), Expect = 7e-07
Identities = 35/35 (100%), Gaps = 0/35 (0%)
Strand=Plus/Minus

Group 4

```
Query 1449 GGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG 1483
          |||
Sbjct 4344 GGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG 4310
```

Score = 68.0 bits (35), Expect = 7e-07
Identities = 45/50 (90%), Gaps = 0/50 (0%)
Strand=Plus/Plus

```
Query 1533 AGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA 1582
          ||| |||
Sbjct 4690 AGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTAGGGTTTA 4739
```

Score = 66.1 bits (34), Expect = 3e-06
Identities = 38/40 (95%), Gaps = 0/40 (0%)
Strand=Plus/Minus

```
Query 1521 GGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTT 1560
          |||
Sbjct 4344 GGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGTATTT 4305
```

Score = 66.1 bits (34), Expect = 3e-06
Identities = 58/70 (82%), Gaps = 0/70 (0%)
Strand=Plus/Minus

```
Query 1425 CCAAGTGTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGA 1484
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 4396 CCAAGGGTTCAGGCTTTTTCCTAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGG 4337

Query 1485 GTTTAAAATT 1494
          ||| |||
Sbjct 4336 GTTTAGAATT 4327
```

Score = 66.1 bits (34), Expect = 3e-06
Identities = 54/64 (84%), Gaps = 0/64 (0%)
Strand=Plus/Minus

```
Query 1590 CCAAGGGTTTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGT 1649
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 4396 CCAAGGGTTCAGGCTTTTTCCTAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGG 4337

Query 1650 GTTT 1653
          |||
Sbjct 4336 GTTT 4333
```

Group 4

Score = 64.1 bits (33), Expect = 1e-05
Identities = 45/51 (88%), Gaps = 0/51 (0%)
Strand=Plus/Plus

```
Query 1287 AAACACTAAACTCTAAACTCTAAATCCTAAACCCTTGGATAAAATACTAAAC 1337
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 172507 AAACCCTAAACCCTAAATTCTAAACCCTAAACCCTTGGATAAATCATAAAC 172557
```

Score = 64.1 bits (33), Expect = 1e-05
Identities = 45/51 (88%), Gaps = 0/51 (0%)
Strand=Plus/Plus

```
Query 1431 GTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTT 1481
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 172651 GTTTAGTATTTATCCAAGGGTTTAGGATTTAGAGTTTAGAGTTTAGTGTTT 172701
```

Score = 60.3 bits (31), Expect = 2e-04
Identities = 39/43 (90%), Gaps = 0/43 (0%)
Strand=Plus/Minus

```
Query 1447 AGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA 1489
        ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4367 AGGGTTTAGTATTTAGAATTTAAGGTTTAGGGTTTAGAATTTA 4325
```

Score = 60.3 bits (31), Expect = 2e-04
Identities = 43/49 (87%), Gaps = 0/49 (0%)
Strand=Plus/Minus

```
Query 1539 TAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAAT 1587
        ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4375 TAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGGGTTTAGAATT 4327
```

Score = 60.3 bits (31), Expect = 2e-04
Identities = 41/46 (89%), Gaps = 0/46 (0%)
Strand=Plus/Plus

```
Query 1444 CCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA 1489
        ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4687 CCAAGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTA 4732
```

Group 4

Score = 60.3 bits (31), Expect = 2e-04
Identities = 39/43 (90%), Gaps = 0/43 (0%)
Strand=Plus/Plus

```
Query 1447 AGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA 1489
          ||||| ||||| ||||| ||||| |||||
Sbjct 4697 AGGGTTTAGTATTTAGAATTTGGGGTTTAGGGTTTAGGGTTTA 4739
```

Score = 60.3 bits (31), Expect = 2e-04
Identities = 65/82 (79%), Gaps = 0/82 (0%)
Strand=Plus/Plus

```
Query 1100 CCCCTAGAGTAAACCTTAAGGTTACCAACCAATAGAAATCACTCATTTACAGTTGATA 1159
          ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 88629 CCCCTAGGATGAACCTTTAGGTTACCAACCAATAGAAAATTGTTATTTTAAATCTAATA 88688
```

```
Query 1160 TCTTTTAAAAAGTAAACAAAA 1181
          ||||| |||||
Sbjct 88689 TCTTTTAATTAAGAAAACAAAA 88710
```

Score = 60.3 bits (31), Expect = 2e-04
Identities = 54/63 (85%), Gaps = 1/63 (1%)
Strand=Plus/Plus

```
Query 1421 TTATCCAAGTGTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTT 1480
          ||| |||| ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 88893 TTACCCAAAGGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGA-TTAGAGTTTAGGGTT 88951
```

```
Query 1481 TAG 1483
          |||
Sbjct 88952 TAG 88954
```

Score = 60.3 bits (31), Expect = 2e-04
Identities = 52/60 (86%), Gaps = 1/60 (1%)
Strand=Plus/Plus

```
Query 1424 TCCAAGTGTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG 1483
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 88985 TCCAAGGGTTTATGGTTTATCCAAGGGTTTAAGGTTTATGA-TTAGAGTTTAGGGTTTAG 89043
```

Score = 60.3 bits (31), Expect = 2e-04
Identities = 47/55 (85%), Gaps = 0/55 (0%)
Strand=Plus/Plus

Group 4

```
Query 2832      GTTGCCCAATTGCCTAATATAAACTTGAGGTGGCCTATTTTCTAATTCAAACCTT 2886
                |||||
Sbjct 175410    GTTGCCCAATTGGCTAATTTAAACTTGAGGTCGCCAATTCCTATTTCAAACCTT 175464
```

Score = 58.4 bits (30), Expect = 6e-04
Identities = 48/57 (84%), Gaps = 0/57 (0%)
Strand=Plus/Plus

```
Query 1526      AGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA 1582
                |||||
Sbjct 4690      AGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTA 4746
```

Score = 58.4 bits (30), Expect = 6e-04
Identities = 40/45 (88%), Gaps = 0/45 (0%)
Strand=Plus/Plus

```
Query 1616      TTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTTTTGACG 1660
                |||
Sbjct 4715      TTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTAGTATTTTCTGACG 4759
```

Score = 58.4 bits (30), Expect = 6e-04
Identities = 96/124 (77%), Gaps = 3/124 (2%)
Strand=Plus/Minus

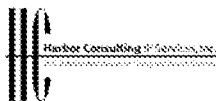
```
Query 1720      TTTTATTTATTTTAAAAACATAATATAACTTGACAATATTTTCTTTTCTTTTAA--AAA 1777
                |||||
Sbjct 88751     TTTTATTTATTTTAAAAGCATAATATAATTTGGCAGGTTATTTTGTCTTCTTAATTAAA 88692

Query 1778      AAATATTAATTATGAAATACTTGATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTA 1837
                |
Sbjct 88691     AGATATTAGATTTAAAATAACAATTTTCTATTGGTT-GGTGAACCTAAAGGTTTCATCCTA 88633
```

```
Query 1838      GGGG 1841
                |||
Sbjct 88632     GGGG 88629
```

Score = 58.4 bits (30), Expect = 6e-04
Identities = 69/81 (85%), Gaps = 4/81 (4%)
Strand=Plus/Plus

```
Query 1496      TCCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAG 1555
                |||||
Sbjct 88878     TCCAAGGGT-TAGGGTTTACCCAAAGGGTTTAGGGTTTA--CCCAAGGGTTTAGGGTTTAG 88934
```



Group 4

```

Query    1556      AATTTAGGGTTTtagggTTTAG    1576
          | | | | | | | | | | | | | | | |
Sbjct    88935    GA-TTAGAGTTTtagggTTTAG    88954

```

Score = 58.4 bits (30), Expect = 6e-04
Identities = 45/50 (90%), Gaps = 1/50 (2%)
Strand=Plus/Minus

Query	1272	TTAATTTTCGTCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCCT	1321
Sbjct	89083	TTAATGTTGTCAACAAAACACTAAACCCTAAACTCT-AATACTAAACCCT	89035

Score = 56.4 bits (29), Expect = 0.002
Identities = 65/83 (78%), Gaps = 0/83 (0%)
Strand=Plus/Plus

Query	1101	CCCTAGAGTAAACCTTAAGGTTACCAACCAATAGAAATCACTCATTTTCACAGTTGATAT	1160
Sbjct	4129	CCCTAAAGTGAACCTCTACATTACCCACCAATAGGAATTAGTTAATTGAGATTGATAT	4188

```
Query    1161    CTTTTAAAAAAGTAAACAAAATA    1183
          |||||
Sbjct    4189    CTTTTAAAAAATGAACCAAATA    4211
```

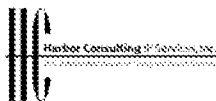
Score = 56.4 bits (29), Expect = 0.002
Identities = 49/59 (83%), Gaps = 0/59 (0%)
Strand=Plus/Plus

Query	1595	GGTTTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTTAAGGTTTAGTGTTT	1653
Sbjct	4673	GGTTCAGGCTTTCCCAAGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTT	4731

Score = 56.4 bits (29), Expect = 0.002
Identities = 35/38 (92%), Gaps = 0/38 (0%)
Strand=Plus/Plus

Query	1523	TTTAGGGTTTTAGGATTTAGGGTTTTAGGGTGTAGAATT	1560
Sbjct	4715	TTTTGGGTTCAGGGTTCAGGGTTCAGGGTTCAGTATC	4752

Score = 56.4 bits (29), Expect = 0.002
Identities = 58/70 (82%), Gaps = 1/70 (1%)
Strand=Plus/Plus



Group 4

Query	544	TTTACCCAATGGTTCTGGA	TTTACCCAAGGGTTCCGGATT	TTAGGATTCAAGGTTTAGAGT	603
Sbjct	88892	TTTACCCAAGGTTTAGGGTT	TTACCCAAGGGTTTAGGGTT	TTAGGATT-AGAGTTTAGGGT	88950
Query	604	TTAGGATTTT	613		
Sbjct	88951	TTAGTATTTT	88960		

Score = 56.4 bits (29), Expect = 0.002
Identities = 35/38 (92%), Gaps = 0/38 (0%)
Strand=Plus/Minus

Query	3838	GATAACCCGTTTAAATTATTTTCAAAATTTTAAAATTT	3875
Subjct	132191	GATAACCCGTTTAAATTATTTTAAATTTTAAATTTT	132154

Score = 54.5 bits (28), Expect = 0.008
Identities = 36/40 (90%), Gaps = 0/40 (0%)
Strand=Plus/Plus

```

Query    1529  GTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTA  1568
          |||||
Sbjct    4565  GTTTAGGGTTTAGGGGTTTCGTGTTTAGAATTTAGGGTTTA  4604

```

Score = 52.6 bits (27), Expect = 0.031
Identities = 47/57 (82%), Gaps = 0/57 (0%)
Strand=Plus/Minus

Query	1121	TTCACCAACCAATAGAAATCACTCATTTTCACAGTTGATATCTTTTAAAAAAGTAAAC	1177
Subject	4909	TTCACCCACCAATAGAAATTAGTTAATTAAGATTTGATATCTCTTAAAAAAGGAAAC	4853

Score = 52.6 bits (27), Expect = 0.031
Identities = 38/41 (92%), Gaps = 1/41 (2%)
Strand=Plus/Minus

Query	1281	TCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCCT	1321
Sbjct	88965	TCAACAAAATACTAAACCCTAAACTCT-AATCCTAAACCCT	88926

Group 4

Score = 50.7 bits (26), Expect = 0.12
Identities = 45/52 (86%), Gaps = 1/52 (1%)
Strand=Plus/Minus

```
Query 1287 AAACACTAAACTCTAAACTCTAAATCCTAAACCCTTGGATAAATACTAAACC 1338
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 88952 AAACCCTAAACTCTAATC-CTAAACCCTAAACCCTTGGGTAAACCCTAAACC 88902
```

Score = 48.8 bits (25), Expect = 0.45
Identities = 46/54 (85%), Gaps = 1/54 (1%)
Strand=Plus/Minus

```
Query 1523 TTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG 1576
          ||||| ||||| ||||| || ||||| || ||||| ||||| ||||| |||||
Sbjct 4507 TTTAGGATTTAGGGTTTAGTATT-AGGGGTTATAATTTAGGGTTTAGGGATTAG 4455
```

Score = 48.8 bits (25), Expect = 0.45
Identities = 27/28 (96%), Gaps = 0/28 (0%)
Strand=Plus/Plus

```
Query 1613 GGGTTTAGGGTTTAGGATTTAGGGTTTA 1640
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4719 GGGTTTAGGGTTTAGGGTTTAGGGTTTA 4746
```

Score = 48.8 bits (25), Expect = 0.45
Identities = 57/68 (83%), Gaps = 2/68 (2%)
Strand=Plus/Minus

```
Query 3450 ATTATAATATTATTATATTACTAATTGCAAAAATTAATTAATACATTATTTTAT-AATAA 3508
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 80053 ATTAAAATAACATTATATTTCTAATCACGAAA-TTAATTAATACATTATCTTATAAACAA 79995
```

```
Query 3509 ATATTTAA 3516
          ||||| |||||
Sbjct 79994 ATATTTAA 79987
```

Score = 48.8 bits (25), Expect = 0.45
Identities = 38/42 (90%), Gaps = 1/42 (2%)
Strand=Plus/Minus

```
Query 3087 TAACAACATATTCATAGATTTTGTGTT-ATCACTTGTTCTGTG 3127
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 158829 TAACAACAGTTTCATAGATTTTTTTTTTATCACTTGTTCTGTG 158788
```

Group 4

Score = 46.8 bits (24), Expect = 1.7
Identities = 34/39 (87%), Gaps = 0/39 (0%)
Strand=Plus/Minus

```
Query 1524 TTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAG 1562
          ||||| ||| ||||| ||||| ||||| |||||
Sbjct 4486 TTAGGGGTTATAATTTAGGGTTTAGGGATTAGGATTTAG 4448
```

Score = 46.8 bits (24), Expect = 1.7
Identities = 30/33 (90%), Gaps = 0/33 (0%)
Strand=Plus/Plus

```
Query 1451 TTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG 1483
          ||| ||||| ||||| ||||| |||||
Sbjct 4715 TTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTAG 4747
```

Score = 46.8 bits (24), Expect = 1.7
Identities = 35/38 (92%), Gaps = 1/38 (2%)
Strand=Plus/Plus

```
Query 1589 TCCAAGGGTTTAGGGTATACCCAAGGGTTTAGGGTTTA 1626
          ||||| ||||| ||||| ||||| |||||
Sbjct 88878 TCCAAGGGTT-AGGGTTTACCCAAGGGTTTAGGGTTTA 88914
```

Score = 46.8 bits (24), Expect = 1.7
Identities = 28/30 (93%), Gaps = 0/30 (0%)
Strand=Plus/Plus

```
Query 1292 CTAAACTCTAAACTCTAAATCCTAAACCCT 1321
          ||||| ||||| ||||| |||||
Sbjct 172433 CTAAACCCTAAACCCTAAATCCTAAACCCT 172462
```

Score = 46.8 bits (24), Expect = 1.7
Identities = 44/54 (81%), Gaps = 0/54 (0%)
Strand=Plus/Plus

```
Query 1500 AGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTT 1553
          ||||| ||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 172648 AGGGTTTAGTATTTATCCAAGGGTTTAGGATTTAGAGTTTAGAGTTTAGTGT 172701
```


Group 4

Score = 46.8 bits (24), Expect = 1.7
Identities = 28/30 (93%), Gaps = 0/30 (0%)
Strand=Plus/Plus

```
Query 1526      AGGGTTTAGGATTTAGGGTTAGGGTTAG 1555
                ||||| ||||| |||||
Sbjct 172667    AGGGTTTAGGATTTAGAGTTAGAGTTAG 172696
```

Score = 44.9 bits (23), Expect = 6.5
Identities = 29/32 (90%), Gaps = 0/32 (0%)
Strand=Plus/Minus

```
Query 1452      TTAGGGTTTAGAATTTAGGGTTAGGGTTAG 1483
                ||||| || ||||| ||||| |||||
Sbjct 4486      TTAGGGGTTATAATTTAGGGTTAGGGATTAG 4455
```

Score = 44.9 bits (23), Expect = 6.5
Identities = 47/59 (79%), Gaps = 0/59 (0%)
Strand=Plus/Plus

```
Query 1438      ATTTATCCAAGGGTTTAGGGTTAGAAATTTAGGGTTAGGGTTAGAGTTTAAATTAT 1496
                |||| || || ||||| || || ||||| ||||| ||||| |||||
Sbjct 4553      ATTTGTCAAAGAGTTTAGGGTTAGGGGTTTCGTGTTTAGAATTTAGGGTTTAAATTAT 4611
```

Score = 44.9 bits (23), Expect = 6.5
Identities = 27/29 (93%), Gaps = 0/29 (0%)
Strand=Plus/Plus

```
Query 1448      GGGTTTAGGGTTTAGAATTTAGGGTTAG 1476
                ||||| ||||| ||||| |||||
Sbjct 4719      GGGTTTAGGGTTTAGGGTTAGGGTTAG 4747
```

Score = 44.9 bits (23), Expect = 6.5
Identities = 108/148 (72%), Gaps = 1/148 (0%)
Strand=Plus/Plus

```
Query 3686      ACTAGGGGTGGGCGTTCGGGTACCTATTCGGGTTTCGGTTCGAGTCTATTCGGATTTCGG 3745
                ||||| |||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 40546     ACTAGGCATGGGTATTCGGGGTCCTAATCGGGTTTCGGTTTTA-TCCATTCAGATTTCGG 40604

Query 3746      ATTTTGGGGTCAAAGATTTAGCCCCATTCGGTTATTTCTAAATTACGGTTCGGGTTTCG 3805
                |||| || || || ||||| ||||| || || ||||| |||||
Sbjct 40605     TTTTTCGGGTTTATCAAAACCAGCCCTATTCGGATTATTTGAAAGTTCGGTTCGGGACCG 40664
```

Group 4

```
Query 3806 GTTCGGATCCTTGCGGATTCGGTTCGGG 3833
          ||||| | | ||| ||||| |||||
Sbjct 40665 GTTCGGGTTTTATCGGGTTCGGGTCGGG 40692
```

Score = 44.9 bits (23), Expect = 6.5
Identities = 33/38 (86%), Gaps = 0/38 (0%)
Strand=Plus/Plus

```
Query 1287 AAACACTAACTCTAACTCTAAATCCTAAACCCTTGG 1324
          |||| ||||| |||| |||| ||||| |||||
Sbjct 172435 AAACCCTAAACCCTAAATCCTAAACCCTAAACCCTTGG 172472
```

- **SEQ 1 from 54-05A application (10/613,053) against the large genomic sequence from Brown Provisional No. 3 (60/308,736)**

Score = 1.640e+04 bits (8528), Expect = 0.0
Identities = 8547/8554 (99%), Gaps = 1/8554 (0%)
Strand=Plus/Minus

```
Query 1 ATTTAAATTTTATACTTAATATGTATTTAAACTCTCCAATGCAATAAGGGATATAAACAA 60
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 174720 ATTTAAATTTTATACTTAATATGTATTTAAACTCTCCAATGCAATAAGGGATATAAACAA 174661

Query 61 AAGGTATTCATAGATGTTATGTATTCGTACACCGATGTATTCGTATACCTTAAATATATG 120
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 174660 AAGGTATTCATAGATGTTATGTATTCGTACACCGATGTATTCGTATACCTTAAATATATG 174601

Query 121 TATACTTATGTATACATATACTTGTGTATTCGTACACCTTAAGTATTCGATGGGTTATGT 180
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 174600 TATACTTATGTATACATATACTTGTGTATTCGTACACCTTAAGTATTCGATGGGTTATGT 174541

Query 181 TGGTATTCGTATATTTTATGTATTTGTACACCTTATGTATACTTATGTATATGTACACCT 240
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 174540 TGGTATTCGTATATTTTATGTATTTGTACACCTTATGTATACTTATGTATATGTACACCT 174481

Query 241 TATGTATTTGTACATCTTAAGTATTAGATGAGTTATGTTGATATTCGTACACCTTATGTA 300
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 174480 TATGTATTTGTACATCTTAAGTATTAGATGAGTTATGTTGATATTCGTACACCTTATGTA 174421

Query 301 TTCGTACACCTTCTGTATACCTTAGGTATTCGTACACCTTAGGTATTTGTACACCTAAGG 360
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 174420 TTCGTACACCTTCTGTATACCTTAGGTATTCGTACACCTTAGGTATTTGTACACCTAAGG 174361

Query 361 TATTCGTACACCTTATGTATACTTATGTATACGTACACCTTATATATTCGAACACCTTAG 420
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 174360 TATTCGTACACCTTATGTATACTTATGTATACGTACACCTTATATATTCGAACACCTTAG 174301
```

Group 4

Query	421	ATATTCGTACATCTTATGTATACGTATACTTATTTCTTGAGTTATAGTGAATTAGATTGT	480
Sbjct	174300	ATATTCGTACATCTTATGTATACGTATACTTATTTCTTGAGTTATAGTGAATTAGATTGT	174241
Query	481	ATTAAACGTTAGACATAGGGTTCCGGATTTATCCAAGGGTTCCAGATTGTTTCAGATTCT	540
Sbjct	174240	ATTAAACGTTAGACATAGGGTTCCGGATTTATCCAAGGGTTCCAGATTGTTTCAGATTCT	174181
Query	541	GGATTTACCCAATGGTTCTGGATTTACCCAAGGGTTCCGGATTTAGGATTCAAGGTTTAG	600
Sbjct	174180	GGATTTACCCAATGGTTCTGGATTTACCCAAGGGTTCCGGATTTAGGATTCAAGGTTTAG	174121
Query	601	AGTTTAGGATTTTAGGTTTAGTGTTTTGTTGATGATTTTTAATATTTAAGATAAATGTAG	660
Sbjct	174120	AGTTTAGGATTTTAGGTTTAGTGTTTTGTTGATGATTTTTAATATTTAAGATAAATGTAG	174061
Query	661	ACAAATTTGTTCTTCCTACCATTTTGACAAAAAATGAAAGATCTATGTAGGTTTCCAAGT	720
Sbjct	174060	ACAAATTTGTTCTTCCTACCATTTTGACAAAAAATGAAAGATCTATGTAGGTTTCCAAGT	174001
Query	721	TTATTAAATTTACCCAGATTTATGAAAATTATCCATAAATTTATATAATTTTATGAATAA	780
Sbjct	174000	TTATTAAATTTACCCAGATTTATGAAAATTATCCATAAATTTATATAATTTTATGAATAA	173941
Query	781	TTTATCATTTATTTGGGTAAATTTTATAAATATGAAAGTTTCTTTTATGGGTCAAAATGT	840
Sbjct	173940	TTTATCATTTATTTGGGTAAATTTTATAAATATGAAAGTTTCTTTTATGGGTCAAAATGT	173881
Query	841	ATAATTTATTCGGATTCTGGATTTACCCAAGGGTTCCGGATTTACCCAAGGATTCCAGAT	900
Sbjct	173880	ATAATTTATTCGGATTCTGGATTTACCCAAGGGTTCCGGATTTACCCAAGGATTCCAGAT	173821
Query	901	TTAGGATTCATGGTTTAGAGTTTAGGAGTTTATGTTTAGTGTTTTGTTGATGATTTTAAA	960
Sbjct	173820	TTAGGATTCATGGTTTAGAGTTTAGGAGTTTATGTTTAGTGTTTTGTTGATGATTTTAAA	173761
Query	961	TATTTAAGATAAGAAGTTTATGCGAGAGAATTTGGTCAAACCTCAGGTTGAGTCTTAACCT	1020
Sbjct	173760	TATTTAAGATAAGAAGTTTATGCGAGAGAATTTGGTCAAACCTCAGGTTGAGTCTTAACCT	173701
Query	1021	CTTAAGACATAAAAAATCACTAGATACTTGACATGGAGGCACCAAATTATCCTATATTTTT	1080
Sbjct	173700	CTTAAGACATAAAAAATCACTAGATACTTGACATGGAGGCACCAAATTATCCTATATTTTT	173641
Query	1081	TGGACTTAATCTTGGTGTACCCCTAGAGTAAACCTTAAGGTTACCAACCAATAGAAATC	1140
Sbjct	173640	TGGACTTAATCTTGGTGTACCCCTAGAGTAAACCTTAAGGTTACCAACCAATAGAAATC	173581
Query	1141	ACTCATTTACAGTTGATATCTTTTAAAAAAGTAAACAAAATATTGTCGAGTTATATTAC	1200
Sbjct	173580	ACTCATTTACAGTTGATATCTTTTAAAAAAGTAAACAAAATATTGTCGAGTTATATTAC	173521

Group 4

Query	1201	ATTTTAAAATAAAAATATTAAAAAATAAAAATAATAATATATGCAAAAAAAGATTTT	1260
Sbjct	173520	ATTTTAAAATAAAAATATTAAAAAATAAAAATAATAATATATGCAAAAAAAGATTTT	173461
Query	1261	TTAAAAAGATTTTAATTTTCGTCAACAAACACTAAACTCTAAACTCTAAATCCTAAACCC	1320
Sbjct	173460	TTAAAAAGATTTTAATTTTCGTCAACAAACACTAAACTCTAAACTCTAAATCCTAAACCC	173401
Query	1321	TTGGATAAATACTAAACCCTAAATTAAAAACATTAAACCATAATAGTATTTTAAAGATTT	1380
Sbjct	173400	TTGGATAAATACTAAACCCTAAATTAAAAACATTAAACCATAATAGTATTTTAAAGATTT	173341
Query	1381	AATGTTTTAGTGTTTAGTGTTTTGATTTAGAATTTAGGATTATCCAAGTGTTTATGATT	1440
Sbjct	173340	AATGTTTTAGTGTTTAGTGTTTTGATTTAGAATTTAGGATTATCCAAGTGTTTATGATT	173281
Query	1441	TATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAAATTATCCAA	1500
Sbjct	173280	TATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAAATTATCCAA	173221
Query	1501	GGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTT	1560
Sbjct	173220	GGGTCTATGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTT	173161
Query	1561	AGGGTTTAGGGTTTAGAGTTTAAAATTATCCAAGGGTTTAGGGTATACCCAAGGGTTTAG	1620
Sbjct	173160	AGGGTTTAGGGTTTAGAGTTTAAAATTATCCAAGGGTTTAGGGTATACCCAAGGGTTTAG	173101
Query	1621	GGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTTTGACGATATTAAAAATAGTTTTCAA	1680
Sbjct	173100	GGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTTTGACGATATTAAAAATAGTTTTCAA	173041
Query	1681	AAATTCATTTTTTGTAACGGCTATTATTTTTTTTTTATATTTTATTTATTTTAAAAACAT	1740
Sbjct	173040	AAATTCATTTTTTGTAACGGCTATTATTTTTTTTTTATATTTTATTTATTTTAAAAACAT	172981
Query	1741	AATATAACTTGACAATATTTTCTTTTCTTTTAAAAAAAATATTAATTATGAAATACTTG	1800
Sbjct	172980	AATATAACTTGACAATATTTTCTTTTCTTTTAAAAAAAATATTAATTATGAAATACTTG	172921
Query	1801	ATTCTATTGGTTGGGTGAACCTAAATGTTCACTCTAGGGGTGAACCTAAGGATAACTCT	1860
Sbjct	172920	ATTCTATTGGTTGGGTGAACCTAAATGTTCACTCTAGGGGTGAACCTAAGGATAACTCT	172861
Query	1861	ATTTTTTGGGGTGAAATAGCACTATAGCGGATATCTTTTTCAATAGATTATAAGCACGGC	1920
Sbjct	172860	ATTTTTTGGGGTGAAATAGCACTATAGCGGATATCTTTTTCAATAGATTATAAGCACGGC	172801
Query	1921	TCTACCTATGACTAATCAAGAACTTGGGATGATTGGAAATCTGCAGGTTGTACTCAATAT	1980
Sbjct	172800	TCTACCTATGACTAGTCAAGAACTTGGGATGATTGGAAATCTGCAGGTTGTACTCAATAT	172741

Group 4

Query	1981	GGGATTATATTGGTTCTAACAAGTAGATATGATCCTTGAAAATTAAAGTTATTAGATCAG	2040
Sbjct	172740	GGGATTATATTGGTTCTAACAAGTAGATATGATCCTTGAAAATTAAAGTTATTAGATCAG	172681
Query	2041	TTCATCGTGAAAGGTGTAGGGTTTGTCAATTTTATTAACAAATTTGTCAATTCATTAACAA	2100
Sbjct	172680	TTCATCGTGAAAGGTGTAGGGTTTGTCAATTTTATTAACAAATTTGTCAATTCATTAACAA	172621
Query	2101	TTTTTGTCAATTTTATAAACATGAAAATTATAACGAATGCACTTTGCTGCCAGATCCCAAT	2160
Sbjct	172620	TTTTTGTCAATTTTATAAACATGAAAATTATAACGAATGCACTTTGCTGCCAGATCCCAAT	172561
Query	2161	TTGTCAATTTTATTTTTGGGAAAAAAATGTAGCATTTTCGTGAGTGTTTCTATTTTTGGCAA	2220
Sbjct	172560	TTGTCAATTTTATTTTTGGGAAAAAAATGTAGCATTTTCGTGAGTGTTTCTATTTTTGGCAA	172501
Query	2221	AAACAAAAAGTGTGAGATCAATTTTGACCAAAAAAAATGTAAGATTCACGTAGGTTTCC	2280
Sbjct	172500	AAACAAAAAGTGTGAGATCAATTTTGACCAAAAAAAATGTAAGATTCACGTAGGTTTCC	172441
Query	2281	AAATTTATTAAATTTACCCAATATATTAAAATTAAATGTAGACAAATTTGTTTTCTGC	2340
Sbjct	172440	AAATTTATTAAATTTACCCAATATATTAAAATTAAATGTAGACAAATTTGTTTTCTGC	172381
Query	2341	CATTTTGGCAAAAAATGAAGGATCTATGAAGGTTTCCAAGTTTATTAAATTTACTCAGAT	2400
Sbjct	172380	CATTTTGGCAAAAAATGAAGGATCTATGAAGGTTTCCAAGTTTATTAAATTTACTCAGAT	172321
Query	2401	TTATGATAATTATCCATAAATTTACATAATTTTATGAATTATCATTTATTTGGGTAGATT	2460
Sbjct	172320	TTATGATAATTATCCATAAATTTACATAATTTTATGAATTATCATTTATTTGGGTAGATT	172261
Query	2461	TCATAAATATGAAAGTTTCTTTTATGAGTCAAAATGTATAATTTATTGGGTAACCTTTCAT	2520
Sbjct	172260	TCATAAATATGAAAGTTTCTTTTATGAGTCAAAATGTATAATTTATTGGGTAACCTTTCAT	172201
Query	2521	AAATTTTAGAATTTACATCGATTTTATATTAATTCGTATAGATTTATGTTGACTTTATAT	2580
Sbjct	172200	AAATTTTAGAATTTACATCGATTTTATATTAATTCGTATAGATTTATGTTGACTTTATAT	172141
Query	2581	ATGAAAAAATATGTATTATATTAAAAGTAGTTGCTCATATATGATTTTTAAATATTAAAT	2640
Sbjct	172140	ATGAAAAAATATGTATTATATTAAAAGTAGTTGCTCATATATGATTTTTAAATATTAAAT	172081
Query	2641	ATGATCCAAAAGTTTAAATGAATAAAGAATGTTTATGGAATTTACAAAAGTTAGTTGTTAA	2700
Sbjct	172080	ATGATCCAAAAGTTTAAATGAATAAAGAATGTTTATGGAATTTACAAAAGTTAGTTGTTAA	172021
Query	2701	AAGTTAGTGGGAAAAAAATTATTTTTTATAGGCAAAGTGGATTTTGGGTCCACGAAATT	2760
Sbjct	172020	AAGTTAGTGGGAAAAAAATTATTTTTTATAGGCAAAGTGGATTTTGGGTCCACGAAATT	171961

Group 4

Query	2761	ACTTTTCCAACCTTGCCAAGTTTAATAGGC AAAAGGTTAAAAATGTCATAAATTTATTCT	2820
Sbjct	171960	ACTTTTCCAACCTTGCCAAGTTTAATAGGC AAAAGGTTAAAAATGTCATAAATTTATTCT	171901
Query	2821	CTCTCTACTAGGTTGCCCAATTGCCTAATATAAACTTGAGGTGGCCTATTTTTCTAATTC	2880
Sbjct	171900	CTCTCTACTAGGTTGCCCAATTGCCTAATATAAAATTTGAGGTGGCCTATTTTCCTAATTC	171841
Query	2881	AAACTTAAAAGTTGCCCTTTCCCCTAATTGACCCATAAAAGAATGAAAGACATTTTTCTT	2940
Sbjct	171840	AAACTTAAAAGTTGCCCTTTCCCCTAATTGACCCATAAAAGAATGAAAGACATTTTTCTT	171781
Query	2941	TTCCAAATTACAATCCCTAGATAATTTTATTTTGTAGGTGCATTCCATCGGTTATGATTA	3000
Sbjct	171780	TTCCAAATTACAATCCCTAGATAATTTTATTTTGTAGGTGCATTCCATCGGTTATGATTA	171721
Query	3001	CAGAATAGCTACGCTTCTCTATTGATTCTTATTGCGCCGTTGGTGACGTTTTCCATGGAA	3060
Sbjct	171720	CAGAATAGCTACGCTTCTCTATTGATTCTTATTGCGCCGTTGGTGACGTTTTCCATGGAA	171661
Query	3061	TCAAGTAGTGTTTTATCTCCTATCACTAACAACATATTCATAGATTTTGTTTATCACTTG	3120
Sbjct	171660	TCAAGTAGTGTTTTATCTCCTATCACTAACAACATATTCATAGATTTTGTTTATCACTTG	171601
Query	3121	TTCTGTGTTCCCTGATCATATACTTGACTCAGTTTCTGTGATTTTCATCAAGTTTTTGAGAA	3180
Sbjct	171600	TTCTGTGTTCCCTGATCATATACTTGACTCAGTTTCTGTGATTTTCATCAAGTTTTTGAGAA	171541
Query	3181	CAGAAGAAGCAAAAAAGAAAACGAGCAGAGCTGCTCTTACAATGTTTTAACCGTGAGTGA	3240
Sbjct	171540	CAGAAGAAGCAAAAAAGAAAACGAGCAGAGCTGCTCTTACAATGTTTTAACCGTGAGTGA	171481
Query	3241	TAAATTTATTTACATAAAAGTATTTTAAAAATAGATTTAATCAACCAATTTAATATATTA	3300
Sbjct	171480	TAAATTTATTTACATAAAAGTATTTTAAAAATAGATTTAATCAACCAATTTAATATATTA	171421
Query	3301	TTTTATATTTAGTTCATTTTTTTTTTGACATCTTTTATATTTAGTTTAGAACACCTCTATT	3360
Sbjct	171420	TTTTATATTTAGTTCATTTTTTTTTTGACATCTTTTATATTTAGTTTAGAACACCTCTATT	171361
Query	3361	TGAGTACAACATAGATTATAATGATAAATTTATAAAATAGCATAATTTTTTATTTTCATT	3420
Sbjct	171360	TGAGTACAACATAGATTATAATGATAAATTTATAAAATAGCATAATTTTTTATTTTCATT	171301
Query	3421	GTTTTATGATAAAATTCTAAATAACAATAATTATAATATTATTATATTACTAATTGCAAA	3480
Sbjct	171300	GTTTTATGATAAAATTCTAAATAACAATAATTATAATATTATTATATTACTAATTGCAAA	171241
Query	3481	AATTAATTAATACATTATTTTATAATAAATATTTAAAACGTTGGGTAGGATTTTGTTAGA	3540
Sbjct	171240	AATTAATTAATACATTATTTTATAATAAATATTTAAAACGTTGGGTAGGATTTTGTTAGA	171181

Group 4

Query	3541	TTTTTTTCAACAAATTTTGTTATAGCTAAAATAAAATTCAAATGTATTGTTAAAATTGAT	3600
Sbjct	171180	TTTTTTTCAACAAATTTTGTTATAGCTAAAATAAAATTCAAATGTATTGTTAAAATTGAT	171121
Query	3601	TTTTTTTTTTTTTTGATTATTAAGATTTAATATAAAATAAACATATATGTCATATTAAATAT	3660
Sbjct	171120	TTTTTTTTTTTTTTGATTATTAAGATTTAATATAAAATAAACATATATGTCATATTAAATAT	171061
Query	3661	TTAACTAAGTGGTCCTAATCTTTGAACTAGGGGTGGGCGTTCGGGTACCTATTCGGGTTT	3720
Sbjct	171060	TTAACTAAGTGGTCCTAATCTTTGAACTAGGGGTGGGCGTTCGGGTACCTATTCGGGTTT	171001
Query	3721	CGGTTTCGAGTCTATTCGGATTTTCGGATTTTGGGGTCAAAGATTTTAGCCCCATTCGGTT	3780
Sbjct	171000	CGGTTTCGAGTCTATTCGGATTTTCGGATTTTGGGGTCAAAGATTTTAGCCCCATTCGGTT	170941
Query	3781	ATTTCTAAATTACGGTTCGGGTTCGGTTCGGATCCTTGCGGATTCGGTTCGGGTTCGGAT	3840
Sbjct	170940	ATTTCTAAATTACGGTTCGGGTTCGGTTCGGATCCTTGCGGATTCGGTTCGGGTTCGGAT	170881
Query	3841	AACCCGTTTAAATTATTTTCAAATTTTAAAATTTCAATTATATATTTTAACTTTTCGAA	3900
Sbjct	170880	AACCCGTTTAAATTATTTTCAAATTTTAAAATTTCAATTATATATTTTAACTTTTCGAA	170821
Query	3901	ATTTGTAAACAAAATAATATATTACATATAAAATTTCAATAATATGTGTCGAAGTACCAAA	3960
Sbjct	170820	ATTTGTAAACAAAATAATATATTACATATAAAATTTCAATAATATGTGTCGAAGTACCAAA	170761
Query	3961	ACTTAACATGTAAATTGGTTTGATTTGGATATTTGGATAGAAAATCAATCATATTTTATA	4020
Sbjct	170760	ACTTAACATGTAAATTGGTTTGATTTGGATATTTGGATAGAAAATCAATCATATTTTATA	170701
Query	4021	TATTTTTGGTGTTTTGAGTATGCTTTAACTATTTATACATGTACTTTTAAATGTTTTAT	4080
Sbjct	170700	TATTTTTGGTGTTTTGAGTATGCTTTAACTATTTATACATGTACTTTTAAATGTTTTAT	170641
Query	4081	ATATTTTCTAGTATTTTGAACAATTTAAAAGTATTATATATATTTTAGATGCTTTTAAAT	4140
Sbjct	170640	ATATTTTCTAGTATTTTGAACAATTTAAAAGTATTATATATATTTTAGATGCTTTTAAAT	170581
Query	4141	ATATATTCAATCTAAAAATAGTTAAATATATATGTATATTAATCTATTTTCGGATACATTC	4200
Sbjct	170580	ATATATTCAATCTAAAAATAGTTAAATATATATGTATATTAATCTATTTTCGGATACATTC	170521
Query	4201	GGATATCCAAAATATTTTGGTTCGGATCGGGTTCGGTTTTGGTTCTTTAAATACCAAAAA	4260
Sbjct	170520	GGATATCCAAAATATTTTGGTTCGGATCGGGTTCGGTTTTGGTTCTTTAAATACCAAAAA	170461
Query	4261	TTTAAACCTATTCGGATATTCAATTAATTTTCGGTTCGGATTTGGTATTACTTTTCAGAT	4320
Sbjct	170460	TTTAAACCTATTCGGATATTCAATTAATTTTCGGTTCGGATTTGGTATTACTTTTCAGAT	170401

Group 4

Query	4321	CGGATTCGGTTCGGTTCCTTTGGATTTCAGTTTTTTTTGTCCAGCCCTACTCTGAACAGTAGA	4380
Sbjct	170400	CGGATTCGGTTCGGTTCCTTTGGATTTCAGTTTTTTTTGTCCAGCCCTACTCTGAACAGTAGA	170341
Query	4381	TAAAAAATAGAACCCTAAATTAATAGGTTAGATTTTGGTTAGGTCTTTCTAATTAGTATG	4440
Sbjct	170340	TAAAAAATAGAACCCTAAATTAATAGGTTAGATTTTGGTTAGGTCTTTCTAATTAGTATG	170281
Query	4441	GAGATTCTCGATTCTCTCATTGCAGTGTGGTATGTCCAACCTCATTGTTTATGTACATA	4500
Sbjct	170280	GAGATTCTCGATTCTCTCATTGCAGTGTGGTATGTCCAACCTCATTGTTTATGTACATA	170221
Query	4501	TCCAATTTAGTTTTGAGTCAAATGTTTAGTTACTTAAGAGTTGAATGAAATAGGGGATGA	4560
Sbjct	170220	TCCAATTTAGTTTTGAGTCAAATGTTTAGTTACTTAAGAGTTGAATGAAATAGGGGATGA	170161
Query	4561	TATTGATGGCCAAGGTTCTCCCAAAGTAAAT-AACCTTTGTTTATATTTTAAGTTAGCTTA	4619
Sbjct	170160	TATTGATGGCCAAGGTTCTCCCAAAGTAAATAAACTTTGTTTATATTTTAAGTTAGCTTA	170101
Query	4620	TAACATCAATAAAAAATGTCATTAACCTGGTTCAATAAAAAATGTCATTAACCTGGTTCCTCTA	4679
Sbjct	170100	TAACATCAATAAAAAATGTCATTAACCTGGTTCAATAAAAAATGTCATTAACCTGGTTCCTCTA	170041
Query	4680	ATATAATTATTTAACACACCTGGCTGTTGATAAATTTTTATGATCGTTTAATAATTTTAG	4739
Sbjct	170040	ATATAATTATTTAACACACCTGGCTGTTGATAAATTTTTATGATCGTTTAATAATTTTAG	169981
Query	4740	AAGTGGATAGTCTGTAAATGGTCTTTGATTGGTCGTCTTGATTTTTAAAAGTGGACTAAA	4799
Sbjct	169980	AAGTGGATAGTCTGTAAATGGTCTTTGATTGGTCGTCTTGATTTTTAAAAGTGGACTAAA	169921
Query	4800	CAAGAAGGCTTAGTAATAAATACTGAACCGGAACTCTACTGGTTTCAATAGCTCGGTTTA	4859
Sbjct	169920	CAAGAAGGCTTAGTAATAAATACTGAACCGGAACTCTACTGGTTTCAATAGCTCGGTTTA	169861
Query	4860	TCAATTTCTCTCGGCTCTGGGTTTAGTGAATCATGTGGCCCTGTGGGTTTAAACAAGGAA	4919
Sbjct	169860	TCAATTTCTCTCGGCTCTGGGTTTAGTGAATCATGTGGCCCTGTGGGTTTAAACAAGGAA	169801
Query	4920	CTCAATCAATCAACTGGTGACAAATCTGAACCGGAAATTGTATAATTCAAACCTGAACCGG	4979
Sbjct	169800	CTCAATCAATCAACTGGTGACAAATCTGAACCGGAAATTGTATAATTCAAACCTGAACCGG	169741
Query	4980	TTCTTGTA AAAACAAATGGAACCCGTTTGTACTTTATCTCTCGTTTATTTTCTCAGTCACG	5039
Sbjct	169740	TTCTTGTA AAAACAAATGGAACCCGTTTGTACTTTATCTCTCGTTTATTTTCTCAGTCACG	169681
Query	5040	AGTTTTTTTTTAGAGATCGACGAAGAACAAAATTTAGGCGAAACAAAATAAAATGTTGGC	5099
Sbjct	169680	AGTTTTTTTTTAGAGATCGACGAAGAACAAAATTTAGGCGAAACAAAATAAAATGTTGGC	169621

Group 4

Query	5100	TAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGATTGTTCTG	5159
Sbjct	169620	TAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGATTGTTCTG	169561
Query	5160	TACGAGATCGATTTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAAGCAGGTTT	5219
Sbjct	169560	TACGAGATCGATTTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAAGCAGGTTT	169501
Query	5220	TGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTAGAGGATGC	5279
Sbjct	169500	TGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTAGAGGATGC	169441
Query	5280	GATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTTGATTTCTG	5339
Sbjct	169440	GATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTTGATTTCTG	169381
Query	5340	TAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCTCTCTATCA	5399
Sbjct	169380	TAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCTCTCTATCA	169321
Query	5400	GAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAATATTCTGATAAAATG	5459
Sbjct	169320	GAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAATATTCTGATAAAATG	169261
Query	5460	TTTCTGCAGCTGCTCTAAGCTCCCCCTTTGCTTTGTCTACATTTGGTAAGATCACCAAGCT	5519
Sbjct	169260	TTTCTGCAGCTGCTCTAAGCTCCCCCTTTGCTTTGTCTACATTTGGTAAGATCACCAAGCT	169201
Query	5520	TGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGA	5579
Sbjct	169200	TGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGA	169141
Query	5580	TAGGGTTTCTGAAGCCTTGATTTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAA	5639
Sbjct	169140	TAGGGTTTCTGAAGCCTTGATTTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAA	169081
Query	5640	TGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCTGAAGC	5699
Sbjct	169080	TGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCTGAAGC	169021
Query	5700	CGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGG	5759
Sbjct	169020	CGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGG	168961
Query	5760	AACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAG	5819
Sbjct	168960	AACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAG	168901
Query	5820	GAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGA	5879
Sbjct	168900	GAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGA	168841

Group 4

Query	5880	TAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGA	5939
Sbjct	168840	TAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGA	168781
Query	5940	GAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTC	5999
Sbjct	168780	GAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTC	168721
Query	6000	TGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGCCC	6059
Sbjct	168720	TGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGCCC	168661
Query	6060	TGATGTTGTAACCTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTTGA	6119
Sbjct	168660	TGATGTTGTAACCTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTTGA	168601
Query	6120	GGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACATA	6179
Sbjct	168600	GGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACATA	168541
Query	6180	TAGTTCAATGATCGATGGATTTTGC AAACAGAATCGTCTTGATGCTGCTGAGCACATGTT	6239
Sbjct	168540	TAGTTCAATGATCGATGGATTTTGC AAACAGAATCGTCTTGATGCTGCTGAGCACATGTT	168481
Query	6240	TTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATAGA	6299
Sbjct	168480	TTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATAGA	168421
Query	6300	CGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTCTCCATGAGATGACTGA	6359
Sbjct	168420	CGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTCTCCATGAGATGACTGA	168361
Query	6360	AACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTACGGGTTCTATCTGGT	6419
Sbjct	168360	AACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTACGGGTTCTATCTGGT	168301
Query	6420	GGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC	6479
Sbjct	168300	GGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC	168241
Query	6480	TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAACTAAAAGA	6539
Sbjct	168240	TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAACTAAAAGA	168181
Query	6540	TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC	6599
Sbjct	168180	TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC	168121
Query	6600	CTTCAATGGTGTGGAACCTGATGTTCAAACCTTACAATATATTGATCAGCGGCTTGATCAA	6659
Sbjct	168120	CTTCAATGGTGTGGAACCTGATGTTCAAACCTTACAATATATTGATCAGCGGCTTGATCAA	168061

Group 4

Query	6660	TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT	6719
Sbjct	168060	TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT	168001
Query	6720	CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA	6779
Sbjct	168000	CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA	167941
Query	6780	TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGAC	6839
Sbjct	167940	TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGAC	167881
Query	6840	CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT	6899
Sbjct	167880	CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT	167821
Query	6900	TTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT	6959
Sbjct	167820	TTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT	167761
Query	6960	TTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGAT	7019
Sbjct	167760	TTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGAT	167701
Query	7020	TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG	7079
Sbjct	167700	TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG	167641
Query	7080	TAAAGAGGAAGTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATGAGTATGGTATG	7139
Sbjct	167640	TAAAGAGGAAGTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATGAGTATGGTATG	167581
Query	7140	TAAGTTTCTGTTTCAGTCTATGTATTTTTTATATAACAAGAATGTATACATTCTTTTGTG	7199
Sbjct	167580	TAAGTTTCTGTTTCAGTCTATGTATTTTTTATATAACAAGAATGTATACATTCTTTTGTG	167521
Query	7200	TGTAGCTTCAGATTGATGATACACGTTCTGGAATTAACCATTGGTTTGGTTTGCATTGT	7259
Sbjct	167520	TGTAGCTTCAGATTGATGATACACGTTCTGGAATTAACCATTGGTTTGGTTTGCATTGT	167461
Query	7260	AGGATCTATCATTTGGGGGATGAATGATCAAAGATTTTCTTCTGTTTGCGCAGCAGAGCT	7319
Sbjct	167460	AGGATCTATCATTTGGGGGATGAATGATCAAAGATTTTCTTCTGTTTGCGCAGCAGAGCT	167401
Query	7320	TCAATGTCATTTTGTCTGCTGCTGCATGTATACCCTACTAATGTTTGATCAAATCGTT	7379
Sbjct	167400	TCAATGTCATTTTGTCTGCTGCTGCATGTATACCCTACTAATGTTTGATCAAATCGTT	167341
Query	7380	GAATAGAGTGATCATAGTGAAAAATTGTGTGGTTAGTAAGTTATTTTGCTGCTATTCTAA	7439
Sbjct	167340	GAATAGAGTGATCATAGTGAAAAATTGTGTGGTTAGTAAGTTATTTTGCTGCTATTCTAA	167281

Group 4

Query	7440	TGACAGCCTTTTATGCGTCTATTGTCTGGGCTTAATAAATTTGACCATTTCCAATTAAAT	7499
Sbjct	167280	TGACAGCCTTTTATGCGTCTATTGTCTGGGCTTAATAAATTTGACCATTTCCAATTAAAT	167221
Query	7500	TCCATACACTTGTTTCACGCAAGATTATTGGTCTGAACTAAAGAGGCACACCTTCCAGAA	7559
Sbjct	167220	TCCATACACTTGTTTCACGCAAGATTATTGGTCTGAACTAAAGAGGCACACCTTCCAGAA	167161
Query	7560	GATTTTCAGGTGTTAAAGATGTTTAGGTGTCTGCCCCGTTCTGTAGCTGTCACCATGGTTA	7619
Sbjct	167160	GATTTTCAGGTGTTAAAGATGTTTAGGTGTCTGCCCCGTTCTGTAGCTGTCACCATGGTTA	167101
Query	7620	TCGTCAAGCTCGGTCTTCATGAGAGCTGATAGCTGTGATGCCATCTTCCTCCTCTTCTTC	7679
Sbjct	167100	TCGTCAAGCTCGGTCTTCATGAGAGCTGATAGCTGTGATGCCATCTTCCTCCTCTTCTTC	167041
Query	7680	ATATTGGCTCTGTCTCTGCCTTGTCTGCTCCCATGTGGGTTTCAGGAGGAGATCATGTTCTT	7739
Sbjct	167040	ATATTGGCTCTGTCTCTGCCTTGTCTGCTCCCATGTGGGTTTCAGGAGGAGATCATGTTCTT	166981
Query	7740	TTAATCTTGGTGGAAATGTTGTTGTCGCTTATGCTTCTCTGGTTCGCCTCTTGACTTGCT	7799
Sbjct	166980	TTAATCTTGGTGGAAATGTTGTTGTCGCTTATGCTTCTCTGGTTCGCCTCTTGACTTGCT	166921
Query	7800	TAGCTTCATTCTTTATCTCCAAATTGCTATGAAATCAATTTACCATAAGTAGAATAAACT	7859
Sbjct	166920	TAGCTTCATTCTTTATCTCCAAATTGCTATGAAATCAATTTACCATACGTAGAATAAACT	166861
Query	7860	TGCAGATTCAATTCTATTATTGCTTAAGCTTTTGTTAATCAACAAAGAAACCAGAGACGAG	7919
Sbjct	166860	TGCAGATTCAATTCTATTATTGCTTAAGCTTTTGTTAATCAACAAAGAAACCAGAGACGAG	166801
Query	7920	AAATACAAACTCTATAAGCTTCTCTTTTTTCTTTCTTGATAGTAAAACCGGTTAGAGAGT	7979
Sbjct	166800	AAATACAAACTCTATAAGCTTCTCTTTTTTCTTTCTTGATAGTAAAACCGGTTAGAGAGT	166741
Query	7980	AGAGATTGATCATATGAACTAAAAATCGATACTAAAACGGTTTGGCTCCGACTTATAAAC	8039
Sbjct	166740	AGAGATTGATCATATGAACTAAAAATCGATACTAAAACGGTTTGGCTCCGACTTATAAAC	166681
Query	8040	CGGAACCCACCGTTTTGCATCTCTCTCTCAAACATCACACAATGTCCAAGATGAAGAAG	8099
Sbjct	166680	CGGAACCCACCGTTTTGCATCTCTCTCTCAAACATCACACAATGTCCAAGATGAAGAAG	166621
Query	8100	TATTTGTGTTGTCATCTCTCTGGGTGAGGAGATGCAAATGTTATATTCTAATTGTTTTCA	8159
Sbjct	166620	TATTTGTGTTGTCATCTCTCTGGGTGAGGAGATGCAAATGTTATATTCTAATTGTTTTCA	166561
Query	8160	GTGCTTGGTCTAACTTTTTTAAGAGATTACTCCAGTGGTTGGATCAAAGAAAGAGTCAA	8219
Sbjct	166560	GTGCTTGGTCTAACTTTTTTAAGAGATTACTCCAGTGGTTGGATCAAAGAAAGAGTCAA	166501

Group 4

Query	8220	CATTGCATTGTGTAAGGTGACGAAAACCTGAGTTAAAGTAAGTGAGAACAATACTTCAATG	8279
Sbjct	166500	CATTGCATTGTGTAAGGTGACGAAAACCTGAGTTAAAGTAAGTGAGAACAATACTTCAATG	166441
Query	8280	CTTTTCTTGTGACAACCTGTGTAATCATCGCATTGGAATATATATGTATATGATGCTTAT	8339
Sbjct	166440	CTTTTCTTGTGACAACCTGTGTAATCATCGCATTGGAATATATATGTATATGATGCTTAT	166381
Query	8340	GATGAAGCTATGAGAATAGGCAAATAGGGTCTGTGTTATTTCCCTGCGATTCTAGATTCT	8399
Sbjct	166380	GATGAAGCTATGAGAATAGGCAAATAGGGTCTGTGTTATTTCCCTGCGATTCTAGATTCT	166321
Query	8400	GATTTGTTTTTCTTCTTAATATTTAGATTAGGTGGTCTTGCTTATCCTGTTTTAGTATT	8459
Sbjct	166320	GATTTGTTTTTCTTCTTAATATTTAGATTAGGTGGTCTTGCTTATCCTGTTTTAGTATT	166261
Query	8460	AGAGTCGGAGTTTTGGGGATGAATCATCCCGGATGATATATACAATTGTGTATTTTATGA	8519
Sbjct	166260	AGAGTCGGAGTTTTGGGGATGAATCATCCCGGATGATATATACAATTGTGTATTTTATGA	166201
Query	8520	ATTTTCAGTTTTTAGTGGATAATGAACACGTTAAC	8553
Sbjct	166200	ATTTTCAGTTTTTAGTGGATAATGAACACGTTAAC	166167

Score = 2963 bits (1541), Expect = 0.0
 Identities = 1885/2052 (91%), Gaps = 18/2052 (0%)
 Strand=Plus/Minus

Query	5090	AAATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTCTCTGCTGAGTCTGCGGCTA	5149
Sbjct	161878	AAATGTTGGCTAGGGTTTGCAGATTTCGAGTCTTCTCTCTCGTCTTCTGTGTCTGCGGCTA	161819
Query	5150	GATTGTTCTGTACGAGATCGATTTCGTGATACTCTGGCCAAGGCAAGC-----GGAGAGA	5203
Sbjct	161818	GATTTTTCTGTACGGGATCGATTTCGTATGCTCTGGCCGAGAAAAGCAGGGATGGAGAGA	161759
Query	5204	GTTGCGAAGCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCA	5263
Sbjct	161758	GTGGCGAAGCAGGTTTTAGAGGAGAGAGTTTGAAGCTGCGAAGTGGATCTTATGAAATCA	161699
Query	5264	AAGGTTTAGAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTT	5323
Sbjct	161698	AAGGGTTAGAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTT	161639
Query	5324	CTGTGGTTGATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCCGGATCTTG	5383
Sbjct	161638	CTGTGATTGATTTCAACAAGCTAATGGGTGCGGTGGTGAGAATGGAACGCCCCGGATCTTG	161579
Query	5384	TGATTTCTCTCTATCAGAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCA	5443
Sbjct	161578	TGATTTCTCTCTATCAAAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCA	161519

Group 4

Query	5444	ATATTCTGATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCCTTTGCTTTGTCTACATTTG	5503
Sbjct	161518	CCATTCTGATAAAATGTTTCTGCAGTTGCTCTAAGCTCCCCCTTTGCTTTGTCTACATTTG	161459
Query	5504	GTAAGATCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATG	5563
Sbjct	161458	GTAAGCTCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCACG	161399
Query	5564	GATTATGTGTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAA	5623
Sbjct	161398	GATTATGTCTTGATCACAGGGTTTCTGAAGCCTTGGATTTGTTTCATCAAATTT-----	161345
Query	5624	CGACATGTAGGCCCAATGTCGTAACCTTCACCACCTTGTATGAACGGTCTTTGCCGCGAGG	5683
Sbjct	161344	-----GTAGACCAGATGTCCTAACGTTTCACCACGCTGATGAATGGTCTTTGCCGCGAGG	161291
Query	5684	GTAGAATTGTGCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTA	5743
Sbjct	161290	GTCGAGTTGTGCGAAGCCGTAGCTCTGCTTGATCGGATGGTGGAAAATGGTCTCCAGCCTG	161231
Query	5744	CCCAGATTACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTG	5803
Sbjct	161230	ACCAGATTACTTACGGAACATTTGTAGATGGGATGTGTAAGATGGGCGACACTGTGTCTG	161171
Query	5804	CACTGAATCTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATAACCAATGTTGTAATCT	5863
Sbjct	161170	CATTGAATCTTCTGAGGAAGATGGAGGAGATAAGCCACATCAAACCAATGTGGTTATCT	161111
Query	5864	ATAGTGCAATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTT	5923
Sbjct	161110	ATAGTGCCATCATTGATGGCCTTTGTAAAGATGGACGCCATAGCGATTCTCATAATCTTT	161051
Query	5924	TCCTGAAATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAG	5983
Sbjct	161050	TCATTGAAATGCAAGACAAGGGAATCTTTCCAAATATAGTTACCTACAACGTATGATCG	160991
Query	5984	TTGGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAG	6043
Sbjct	160990	GTGGATTTTGCATCTCTGGTAGATGGAGTGCAGCCAGCGGTTGTTGCAAGAAATGTTAG	160931
Query	6044	AAAGGAAGATCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGG	6103
Sbjct	160930	AAAGGAAGATCAGCCCTAATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGG	160871
Query	6104	AAGGCAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCC	6163
Sbjct	160870	AAGGCAAGTTCTTCGAGGCTGCAGAATTATACGATGAGATGCTTCCAAGGGGTATCATTC	160811
Query	6164	CTAATACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATG	6223
Sbjct	160810	CTAATACAATCACATATAATTCAATGATCGATGGGTTTTGCAAACAGGATCGTCTTGATG	160751

Group 4

Query	6224	CTGCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTT	6283
Sbjct	160750	CTGCTGAGGACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGGACGTATTCACCTT	160691
Query	6284	TCAATACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTC	6343
Sbjct	160690	TCACTACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTC	160631
Query	6344	TCCATGAGATGACTGAAACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTC	6403
Sbjct	160630	TCCATGAGATGCCTAGAAGAGGATTAGTTGCTAACACAGTTACTTACAACACTCTTATTC	160571
Query	6404	ACGGGTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCT	6463
Sbjct	160570	ACGGGTTCTGTCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAGCAGATGATTT	160511
Query	6464	CTAGTGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATA	6523
Sbjct	160510	CTAGTGGTGTGTGCCCTGATATCGTTACTTGTAACTTTGCTGGACGGTCTCTGCGATA	160451
Query	6524	ATGGGAAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATC	6583
Sbjct	160450	ATGGGAAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTAAGATGGATC	160391
Query	6584	TTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTACAATATATTGA	6643
Sbjct	160390	TTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCTAACTTACAATATATTGA	160331
Query	6644	TCAGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGC	6703
Sbjct	160330	TCTGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGC	160271
Query	6704	CCCACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCA	6763
Sbjct	160270	CACACAGAGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGACTATGCA	160211
Query	6764	AGCAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCT	6823
Sbjct	160210	AGCAGAGCCGCCTAGATGAGGCTACACAAATGTTTGTTTCGATGGGTAGCAAGAGCTTCT	160151
Query	6824	CTCCAAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTG	6883
Sbjct	160150	CTCCCAACGTAGTGACATTTAACACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTG	160091
Query	6884	ATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTA	6943
Sbjct	160090	ATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTGATGCAATTA	160031
Query	6944	CTTACATCACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACA	7003
Sbjct	160030	TTTACATCACTTTGATTTATGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACA	159971

Group 4

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Query 7004      TTTTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGC 7063
                |||
Sbjct 159970    TTTTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGC 159911

Query 7064      TGACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGC 7123
                |||
Sbjct 159910    TGACTGGTTTATGGAGTAAAGAGGAACTAGAAAGGGCAGTGGCAATGCTTGAGGATCTGC 159851

Query 7124      AGATGAGTATGG 7135
                |||
Sbjct 159850    AGATGAGTGTGG 159839

```

Score = 2807 bits (1460), Expect = 0.0
Identities = 1966/2199 (89%), Gaps = 56/2199 (2%)
Strand=Plus/Minus

```

Query 4940      CAAATCTGAACCGGAAATTGTATAATTCAAATGAACCGGTTCTTGTAACAAATGGAA 4999
                |||
Sbjct 178525    CAACTCTGAACCGGAAATTGTATAATTCAAATGAACCGGTTGTTGTAAATCAAATGGAA 178466

Query 5000      CCCGTTTGTACTTTATCTCTCGTTTATTTTCTCAGTCACGAGTTTTTTTAGAGATCGAC 5059
                || ||| |||
Sbjct 178465    CCGGTTT--ACT-----AGCCACTCAGTCGAGAGTGGTTTT-AGAGATCGAC 178422

Query 5060      GAAGAACAAAATTTAGGCGAAACAAAATAAAATGTTGGCTAGGGTTTGTGGATTCAAGT 5119
                |||
Sbjct 178421    GAAGAACAAAGTTCAGGCGAAGCAAAAAT-----GTTGGCTAGGGTTTATAGATCCGGAT 178367

Query 5120      GTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGATTGTTCTGTACGAGATCGATTTCGTGATA 5179
                |||
Sbjct 178366    CTTCTTCTTCTCCTGCTGTGTCTGCGGCTAGATTGTTCTGTACGAGATCGATTTCGTGATA 178307

Query 5180      CTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAAGCAGGTTTTGGAGGAGAGAGTTTGAAGC 5239
                |||
Sbjct 178306    CTCTGGCCAAGAAAAGCAGGGA---TGGAGAGAGTGGTTTTGGAGGAGAGAGTTTGAAGC 178250

Query 5240      TGCAAAGTGGGTTTCATGAAATCAAAGGTTTAGAGGATGCGATTGATTTGTTTCAGTGACA 5299
                |||
Sbjct 178249    TGCGAAGCGGATTTACGAAATCAAAGGTTAGAAGATGCGATTGATTTGTTTCGGTGATA 178190

Query 5300      TGCTTCGATCTCGTCCTTTACCTTCTGTGGTTGATTTCTGTAAATTGATGGGTGTGGTGG 5359
                |||
Sbjct 178189    TGGTACGATCTCGTCCTTTACCTTCTGTAAATTGATTTCTGTAAATTGATGGGAGTTGTGG 178130

Query 5360      TGAGAATGGAACGCCCGGATCTTGTGATTTCTCTCTATCAGAAGATGGAAAGGAAACAGA 5419
                |||
Sbjct 178129    TGAGGATGGGAAGGCTCGATGTTGTGATTTCTCTCCATAGGAAGATGGAAATGAGGCGGG 178070

Query 5420      TTCGATGTGATATATACAGCTTCAATATTCTGATAAAATGTTTCTGCAGCTGCTCTAAGC 5479
                |||
Sbjct 178069    TTCCATGTAACGCATACAGCTTCAACATCCTGATGAAGTGTCTGCAGCTGCTCTAAGC 178010

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Group 4

Query	6257	AGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATAGACGGATATTGTGGGGCTA	6316
Sbjct	177258	AGGGCTGCTCTCCGGACATAATCACTTTCAATACTCTCATAGCCGGATACTGTAGAGCTA	177199
Query	6317	AGAGGATAGATGATGGAATGGAACCTTCTCCATGAGATGACTGAAACAGGATTAGTTGCTG	6376
Sbjct	177198	AGAGGGTAGATGATGGAATAAACTTCTCCATGAGATGACTGAAGCAGGATTAGTTGCTA	177139
Query	6377	ACACAACACTTACAACACTCTTATTACGGGTTCTATCTGGTGGGCGATCTTAATGCTG	6436
Sbjct	177138	ACACAATTACTTACACCACTCTTATTACGGGTTCTGTGAGGTGGGCGATCTTAATGCTG	177079
Query	6437	CTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCCTGATATCGTTACTTGTG	6496
Sbjct	177078	CTCAAGACCTTCTACAGGAGATGGTCTCTAGTGGTGTGTGCCCTAATGTCGTTACTTGTA	177019
Query	6497	ACACTTTGCTGGATGGTCTCTGCGATAATGGGAACTAAAAGATGCATTGGAAATGTTTA	6556
Sbjct	177018	ACACTTTGCTGGACGGTCTCTGCGATAATGGGAACTAAAAGATGCATTGGAAATGTTTA	176959
Query	6557	AGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCCCTTCAATGGTGTGGAAC	6616
Sbjct	176958	AGGCTATGCAGAAGAGTAAGATGGATATTGATGCTAGTCACCCCTTTAATGGTGTGGAAC	176899
Query	6617	CTGATGTTCAAACCTTACAATATATTGATCAGCGGCTTGATCAATGAAGGGAAGTTTTTAG	6676
Sbjct	176898	CTGATGTTCAAACCTTACAATATATTGATCAGTGGCTTGATCAATGAAGGGAAGTTTTTAG	176839
Query	6677	AGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGTCCCAGATACTATCACCT	6736
Sbjct	176838	AGGCCGAGGAATTATACGAGGAGATGCCACACAGAGGTATAGTCCCAGATACTATCACCT	176779
Query	6737	ATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGATGAGGCTACACAAATGT	6796
Sbjct	176778	ATAACTCAGTGATCCATGGTTTATGCAAGCAAAGCCGCCTAGATGAGGCTACACAAATGT	176719
Query	6797	TTGATTTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGACCTTTACTACACTCATTA	6856
Sbjct	176718	TTGATTTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGACCTTTACTACACTCATTA	176659
Query	6857	ATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTC	6916
Sbjct	176658	ATGGATACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTC	176599
Query	6917	GAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGATTTGTGGTTTTTCGTAAAG	6976
Sbjct	176598	GAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGATTCATGGTTTTTCGTAAAG	176539
Query	6977	TGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTATC	7036
Sbjct	176538	TGGGTAATATTAATGGGGCTCTAGATATTTTCCAGGAGATGATGGCAAGTGGTGTGTATC	176479

Group 4

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Query 7037      CTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAA 7096
                |||
Sbjct 176478    CTGATACCATTACTATCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAA 176419

Query 7097      GGGCAGTGGCAATGCTTGAGAACTGCAGATGAGTATGG 7135
                |||
Sbjct 176418    GGGCAGTGGCAATGCTTGAGGATCTGCAGATGAGTGTGG 176380

```

Score = 1698 bits (883), Expect = 0.0
Identities = 1091/1170 (93%), Gaps = 13/1170 (1%)
Strand=Plus/Plus

```

Query 6420      GGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC 6479
                |||
Sbjct 574       GGGCGATCTTAATTCTGCTCAAGACCTTTTACAGGAGATGATTTCTAGTGGTGTGTGCCC 633

Query 6480      TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAACTAAAAGA 6539
                |||
Sbjct 634       TAATGTCGTTACTTGTAACTTTGCTGGACGGTCTCTGCGATCGCGGAACTAAAAGA 693

Query 6540      TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC 6599
                |||
Sbjct 694       TGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTATGATGGACATTGATGCTACTCATGC 753

Query 6600      CTTCAATGGTGTGGAACCTGATGTTCAAACCTACAATATATTGATCAGCGGCTTGATCAA 6659
                |||
Sbjct 754       CTTCAATGGTGTGGAACCTGATGTTCAAACCTACAATATATTGATCAGCGGATTGATTAA 813

Query 6660      TGAAGGGAAGTTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT 6719
                |||
Sbjct 814       TGAAGGGAAGTTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT 873

Query 6720      CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA 6779
                |||
Sbjct 874       CCCAGATACTGTTACCTATAGCTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGA 933

Query 6780      TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGAC 6839
                |||
Sbjct 934       TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGAC 993

Query 6840      CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT 6899
                |||
Sbjct 994       ATTTAACACACTCATTACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCT 1053

Query 6900      TTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT 6959
                |||
Sbjct 1054     TTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAATGCAATTACTTACATCACTTTGAT 1113

Query 6960      TTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGAT 7019
                |||
Sbjct 1114     TCGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGTCTCTAGACATTTTCCAGGAGATGAT 1173

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Group 4

Query	5597	TGGATTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAATGTCGTAACCTTCACCA	5656
Sbjct	78	TGGATTTGTTTCATCAAATGTGTAAA-----CCAAATGTCGTAACCTTCACCA	125
Query	5657	CTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTGCGAAGCCGTAGCTCTGCTTGATC	5716
Sbjct	126	CGCTGATGAACGGTCTTTGCCGCGAGGGTAGAGTTGTGCGAGGCCGTAGCTCTGCTTGATC	185
Query	5717	GGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGGAACAATCGTAGATGGGA	5776
Sbjct	186	GGATGGTAGAAGATGGTCTCCAGCCTAACCAGATTACTTACGGAACAATTGTAGATGGGA	245
Query	5777	TGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAGGAAGATGGAGGAGGTGA	5836
Sbjct	246	TGTGTAAGATGGGAGACACTGTGTCTGCATTGAATCTTCTGAGGAAGATGGAGGAGTTGA	305
Query	5837	GCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGATAGCCTTTGTAAAGACG	5896
Sbjct	306	GCCACATCAAACCGGATGTGGTAATCTATAGTGCCATCATTGATGGCCTTTGGAAAGACG	365
Query	5897	GACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGAGAAAGGAATCTTTCCCG	5956
Sbjct	366	GACGTCATACCGATGCTCAAAATCTTTTCACTGAAATGCAAGACAAGGAATCTTTCCAG	425
Query	5957	ATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTCTGGTAGATGGAGCGACG	6016
Sbjct	426	ATATAGTTACCTACAGCTGTATGATTAATGGATTTTGTAGCTCTGGTAAATGGAGTGAAG	485
Query	6017	CGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGCCCTGATGTTGTAACCTTATA	6076
Sbjct	486	CCCAGCGCTTGTTGCAAGAAATGTTAGTAAGGAAGATCAGCCCTGATGTTGTAACCTTCA	545
Query	6077	ATGCTTTGATCAATGCATTTGTCAAGGAAGGC	6108
Sbjct	546	GTGGATTGATCAATGCATTGGTCAAAGAGGGC	577

Score = 164 bits (85), Expect = 8e-36
 Identities = 128/147 (87%), Gaps = 3/147 (2%)
 Strand=Plus/Plus

Query	7668	CTCCTCTTCTTCATATTGGCTCTGTCCTGCCTTGTCTGCTCCCATGTGGGTTTCAGGAGGA	7727
Sbjct	2657	CTCCTCTTCTTCATATTGGTTCGGTCCGTCCTGCCTTGTCTGCTCCCATGTGGGTTAAGGAGGA	2716
Query	7728	GATCATGTTCTTTTAATCTTGGTGGAAATGTTGTTGTGCGCTTATGCTTCTCTGGTTTCG--	7785
Sbjct	2717	GATCATGTTTTTAAGATCGTGGTGGAAATGTTGGTGTGGTTGTCCTTCGCTGATTTCGCC	2776
Query	7786	-CCTCTTGACTTGCTTAGCTTCATTCT	7811
Sbjct	2777	TCCTCTTGATTTGCTTAGCTTCATTCT	2803

Group 4

Score = 150 bits (78), Expect = 9e-32
Identities = 316/435 (72%), Gaps = 0/435 (0%)
Strand=Plus/Plus

```

Query 6058 CCTGATGTTGTAACCTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTT 6117
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 770 CCTGATGTTCAAACCTTACAATATATTGATCAGCGGATTGATTAATGAAGGGAAGTTTTTA 829

Query 6118 GAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACA 6177
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 830 GAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGTCCCAGATACTGTTACC 889

Query 6178 TATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATG 6237
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 890 TATAGCTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGATGAGGCTACACAAATG 949

Query 6238 TTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATA 6297
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 950 TTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGACATTTAACACACTCATT 1009

Query 6298 GACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTCTCCATGAGATGACT 6357
          || || || || || || || || || || || || || || || || || || || || ||
Sbjct 1010 ACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCTTTTCTGCGAGATGGGT 1069

Query 6358 GAAACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTCACGGGTTCTATCTG 6417
          || || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
Sbjct 1070 CGAAGAGGGATAGTTGCTAATGCAATTACTTACATCACTTTGATTCGTGGTTTTTCGTAAA 1129

Query 6418 GTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGC 6477
          ||| ||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 1130 GTGGGTAATATTAATGGGTCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTAT 1189

Query 6478 CCTGATATCGTTACT 6492
          ||| ||| || ||| |||
Sbjct 1190 CCTGATACCATTACT 1204

```

Score = 144 bits (75), Expect = 5e-30
Identities = 180/225 (80%), Gaps = 3/225 (1%)
Strand=Plus/Plus

```

Query 1099 ACCCCTAGAGTAAACCTTAAGGTTACACC-AACCAATAGAAATCACTCATTTCACAGTTGA 1157
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 172879 ACCCCTAGAGTGAACATTTAGGTTACCCCAACCAATAGGAATCAAGTATTTTATAATTAA 172938

Query 1158 TATCTTTTA-AAAAAGTAAACAAAATATTGTGCGAGTTATATTACATTTTTTAAAATAAAAA 1216
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 172939 TATTTTTTTTTTAAAAGAAAAGAAAATATTGTCAAGTTATATTATGTTTTTTAAAATAAATA 172998

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Group 4

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Query 1217      TATTAAAAAATAAAAAATAATAATATATGCAAAAAAAGATTTTTTAAAAAGATTTTAAT 1276
                | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 172999    AAATATAAAAAAAAAAATAATAGCCGTTACAAAAAATGAATTTTGTAAACTATTTTAAAT 173058

Query 1277      TTCGTCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCCT 1321
                | | | | | | | | | | | | | | | | | | | | | |
Sbjct 173059    ATCGTCAA-AAAACACTAAACCTTAAACCCTAAATCCTAAACCCT 173102

```

Score = 144 bits (75), Expect = 5e-30
 Identities = 180/225 (80%), Gaps = 3/225 (1%)
 Strand=Plus/Plus

```

Query 1619      AGGGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTT-TTGACGATATTAAAAATAGTTTT 1677
                | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 173400    AGGGTTTAGGATTTAGAGTTTAGAGTTTAGTGTTTTGTTGACGAAATTAAAATCTTTTAA 173459

Query 1678      CAAAAATTCATTTTTTTGTAACGGCTATTATTTTTTTTTTTATATTTTATTTATTTTAAAA 1737
                | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 173460    AAAAATCTTTTTTTTTTGCATATATTATTATTTTATTTTAAATATTTTATTTTAAAAA 173519

Query 1738      CATAATATAACTTGACAATATTTTCTTTTCTTTTAAAAAAAATATTAATTATGAAATAC 1797
                | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 173520    TGTAATATAACTCGACAATATTTTGTCTTACTTTTT-TAAAAGATATCAACTGTGAAATGA 173578

Query 1798      TTGATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTAGGGGT 1842
                | | | | | | | | | | | | | | | | | | | | | |
Sbjct 173579    GTGATTTCTATTGGTT-GGTGAACCTTAAGGTTTACTCTAGGGGT 173622

```

Score = 141 bits (73), Expect = 7e-29
 Identities = 107/119 (89%), Gaps = 3/119 (2%)
 Strand=Plus/Minus

```

Query 2918      AAAGAATGAAAGACATTTTTCTTTTCCAAATT-ACAATCCCTAGATAATTTTATTTTGTA 2976
                | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 159685    AAAGAATGAAAGACACTTTTCTTTTCCAAATTTACAAGGCCTTGTTGATTTTATTTTGTA 159626

Query 2977      GGTGCATTCCATCGGTTATGATTACAGAATAGCTACGCTTCTCTATTGATTCTTATTGC 3035
                | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 159625    GGTGAATTCCATCGGTTATGATTATTG--TAGCTACGCTTCTCTATTGATTCTTATTGC 159569

```

Score = 89.1 bits (46), Expect = 3e-13
 Identities = 54/58 (93%), Gaps = 0/58 (0%)
 Strand=Plus/Minus

```

Query 1519      AGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG 1576
                | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 4367      AGGGTTTAGTATTTAGAATTTAAGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG 4310

```

Group 4

Score = 87.2 bits (45), Expect = 1e-12
Identities = 68/77 (88%), Gaps = 2/77 (2%)
Strand=Plus/Minus

```
Query 4413      TTTTGGTTAGGTCTTTCTAATTAGTATGGAGATTCTCGATTCCCTTCTCATTGCAG--TGT 4470
                |||
Sbjct 159216    TTTTGGTTAGGTCTTGCTAATTAGTATGGAGTTGCCTTATTCCTTCTCATTGCAGTGTGT 159157

Query 4471      GGTATGTCCAACATCATT 4487
                |||
Sbjct 159156    GGTATGTCCTACTCATT 159140
```

Score = 85.3 bits (44), Expect = 5e-12
Identities = 56/62 (90%), Gaps = 0/62 (0%)
Strand=Plus/Plus

```
Query 1515      CCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTT 1574
                |||
Sbjct 4686      CCCAAGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTAGGGTTTAGGGTTT 4745

Query 1575      AG 1576
                ||
Sbjct 4746      AG 4747
```

Score = 83.4 bits (43), Expect = 2e-11
Identities = 62/69 (89%), Gaps = 1/69 (1%)
Strand=Plus/Plus

```
Query 1586      TTATCCAAGGGTTTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAAGGTT 1645
                |||
Sbjct 88893     TTACCCAAAGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGA-TTAGAGTTTAGGGTT 88951

Query 1646      TAGTGTTTT 1654
                |||
Sbjct 88952     TAGTATTTT 88960
```

Score = 83.4 bits (43), Expect = 2e-11
Identities = 53/58 (91%), Gaps = 0/58 (0%)
Strand=Plus/Minus

```
Query 3153      TTCTGTGATTTTCATCAAGTTTTTGGAGAACAGAAGAAGCAAAAAGAAAACGAGCAGAG 3210
                |||
Sbjct 159527    TTCTGTGATTTTCATCAAATTTTTAAAAACAGAAAAGCAAGAAGAAAACGAGCAGAG 159470
```


Group 4

Score = 81.4 bits (42), Expect = 7e-11
Identities = 61/68 (89%), Gaps = 1/68 (1%)
Strand=Plus/Plus

```
Query 1493 TTATCCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTT 1552
      ||| |||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 88893 TTACCCAAAGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGA-TTAGAGTTTAGGGTT 88951

Query 1553 TAGAATTT 1560
      ||| ||||
Sbjct 88952 TAGTATTT 88959
```

Score = 73.7 bits (38), Expect = 1e-08
Identities = 70/86 (81%), Gaps = 0/86 (0%)
Strand=Plus/Minus

```
Query 1497 CCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGA 1556
      ||||| ||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4396 CCAAGGGTTCAGGCTTTTTCCTAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGG 4337

Query 1557 ATTTAGGGTTTAGGGTTTAGAGTTTA 1582
      ||||| ||||| ||||| |||||
Sbjct 4336 GTTTAGAATTTAGGGTTTAGGGTTTA 4311
```

Score = 71.8 bits (37), Expect = 5e-08
Identities = 73/86 (84%), Gaps = 2/86 (2%)
Strand=Plus/Plus

```
Query 1496 TCCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAG 1555
      ||||| ||| || ||| || ||||| ||||| ||||| || ||||| ||||| |||||
Sbjct 88985 TCCAAGGTTTATGGTTTATCCAAGGGTTTAAGGTTTATGA-TTAGAGTTTAGGGTTTAG 89043

Query 1556 AATTTAGGGTTTAGGGTTTAGAGTTT 1581
      | |||| ||||| ||||| |||||
Sbjct 89044 TA-TTAGAGTTTAGGGTTTAGTGTTT 89068
```

Score = 68.0 bits (35), Expect = 7e-07
Identities = 39/41 (95%), Gaps = 0/41 (0%)
Strand=Plus/Plus

```
Query 7600 TGTAGCTGTCAACCATGGTTATCGTCAAGCTCGGTCTTCATG 7640
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 2557 TGTAGCTGTCTCCATGGTTATCATCAAGCTCGGTCTTCATG 2597
```

Group 4

Group 4

Score = 66.1 bits (34), Expect = 3e-06
Identities = 54/64 (84%), Gaps = 0/64 (0%)
Strand=Plus/Minus

```
Query 1590 CCAAGGGTTTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGT 1649
          ||||| ||| | | || ||||| ||||| ||||| ||||| |||||
Sbjct 4396 CCAAGGGTTCAGGCTTTTTCCTAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGG 4337

Query 1650 GTTT 1653
          ||||
Sbjct 4336 GTTT 4333
```

Score = 64.1 bits (33), Expect = 1e-05

Identities = 45/51 (88%), Gaps = 0/51 (0%)
Strand=Plus/Plus

```
Query 1287 AAACACTAAACTCTAAACTCTAAATCCTAAACCCTTGGATAAATACTAAAC 1337
          |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 173240 AAACCCTAAACCCTAAATTCTAAACCCTAAACCCTTGGATAAATCATAAAC 173290
```

Score = 64.1 bits (33), Expect = 1e-05
Identities = 45/51 (88%), Gaps = 0/51 (0%)
Strand=Plus/Plus

```
Query 1431 GTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTT 1481
          |||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 173384 GTTTAGTATTTATCCAAGGGTTTAGGATTTAGAGTTTAGAGTTTAGTGTTT 173434
```

Score = 60.3 bits (31), Expect = 2e-04
Identities = 39/43 (90%), Gaps = 0/43 (0%)
Strand=Plus/Minus

```
Query 1447 AGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA 1489
          ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4367 AGGGTTTAGTATTTAGAATTTAAGGTTTAGGGTTTAGAATTTA 4325
```

Score = 60.3 bits (31), Expect = 2e-04
Identities = 43/49 (87%), Gaps = 0/49 (0%)
Strand=Plus/Minus

Group 4

```
Query 1539 TAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAAATT 1587
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4375 TAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGGGTTTAGAATT 4327
```

Score = 60.3 bits (31), Expect = 2e-04
 Identities = 41/46 (89%), Gaps = 0/46 (0%)
 Strand=Plus/Plus

```
Query 1444 CCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA 1489
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4687 CCAAGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTA 4732
```

Score = 60.3 bits (31), Expect = 2e-04
 Identities = 39/43 (90%), Gaps = 0/43 (0%)
 Strand=Plus/Plus

```
Query 1447 AGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA 1489
          ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4697 AGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTAGGGTTTA 4739
```

Score = 60.3 bits (31), Expect = 2e-04
 Identities = 65/82 (79%), Gaps = 0/82 (0%)
 Strand=Plus/Plus

```
Query 1100 CCCCTAGAGTAAACCTTAAGGTTTACCAACCAATAGAAATCACTCATTTACAGTTGATA 1159
          ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 88629 CCCCTAGGATGAACCTTTAGGTTTACCAACCAATAGAAAATTGTTATTTTAAATCTAATA 88688
```

```
Query 1160 TCTTTTAAAAAAGTAAACAAAA 1181
          ||||| |||||
Sbjct 88689 TCTTTTAATTAAGAAAACAAAA 88710
```

Score = 60.3 bits (31), Expect = 2e-04
 Identities = 54/63 (85%), Gaps = 1/63 (1%)
 Strand=Plus/Plus

```
Query 1421 TTATCCAAGTGTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTT 1480
          ||| |||| |||| | |||| ||||| ||||| ||||| |||||
Sbjct 88893 TTACCCAAAGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGA-TTAGAGTTTAGGGTT 88951
```

```
Query 1481 TAG 1483
          |||
Sbjct 88952 TAG 88954
```

Group 4

Score = 60.3 bits (31), Expect = 2e-04
Identities = 52/60 (86%), Gaps = 1/60 (1%)
Strand=Plus/Plus

```
Query 1424   TCCAAGTGTATGATTTATCCAAGGGTTAGGGTTAGAAATTTAGGGTTAGGGTTAG 1483
          |||||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 88985  TCCAAGGTATGATTTATCCAAGGGTTAAGGTTATGA-TTAGAGTTAGGGTTAG 89043
```

Score = 60.3 bits (31), Expect = 2e-04
Identities = 47/55 (85%), Gaps = 0/55 (0%)
Strand=Plus/Plus

```
Query 2832   GTTGCCCAATTGCCTAATATAAACTTGAGGTGGCTATTTTCTAATTCAAACCT 2886
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 176143 GTTGCCCAATTGGCTAATTTAACTTGAGGTGCGCCAATTCCTATTTCAAACCT 176197
```

Score = 58.4 bits (30), Expect = 6e-04
Identities = 48/57 (84%), Gaps = 0/57 (0%)
Strand=Plus/Plus

```
Query 1526   AGGGTTTAGGATTTAGGGTTAGGGTTAGAAATTTAGGGTTAGGGTTAGAGTTTA 1582
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4690   AGGGTTTAGGGTTAGTATTTAGAAATTTGGGTTTAGGGTTAGGGTTAGGGTTTA 4746
```

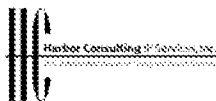
Score = 58.4 bits (30), Expect = 6e-04
Identities = 40/45 (88%), Gaps = 0/45 (0%)
Strand=Plus/Plus

```
Query 1616   TTTAGGGTTTAGGATTTAGGGTTTAAGGTTAGTGTGTTTTTGACG 1660
          |||  ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4715   TTTTGGGTTTAGGGTTAGGGTTAGGGTTAGTATTTTCTGACG 4759
```

Score = 58.4 bits (30), Expect = 6e-04
Identities = 96/124 (77%), Gaps = 3/124 (2%)
Strand=Plus/Minus

```
Query 1720   TTTTATTTATTTTAAAACATAATATAACTTGACAATATTTTCTTTCTTTTAA--AAA 1777
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 88751  TTTTATTTATTTTAAAAGCATAATATAATTTGGCAGGTTATTTTGTCTTAAATAAA 88692

Query 1778   AAATATTAATTATGAAATACTTGATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTA 1837
          |  |||||  |  |||||  ||  ||||| ||||| ||||| ||||| |||||
Sbjct 88691  AGATATTAGATTTAAAATAACAATTTCTATTGGTT-GGTGAACCTAAAGGTTTCATCCTA 88633
```



Group 4

Query	1838	GGGG	1841
Sbjct	88632	GGGG	88629

Score = 58.4 bits (30), Expect = 6e-04
Identities = 69/81 (85%), Gaps = 4/81 (4%)
Strand=Plus/Plus

Query	1496	TCCAAGGGTCTAGGGTATACCCAAGGGTTT	1555
Sbjct	88878	TCCAAGGGT-TAGGGTTTACCCAAAGGTTT	88934
Query	1556	AATTTAGGGTTT	1576
Sbjct	88935	GA-TTAGAGTTT	88954

Score = 58.4 bits (30), Expect = 6e-04
Identities = 45/50 (90%), Gaps = 1/50 (2%)
Strand=Plus/Minus

Query	1272	TTAATTTTCGTCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCCT	1321
Sbjct	89083	TTAATGTTGTCAACAAAACACTAAACCCTAAACTCT-AATACTAAACCCT	89035

Score = 56.4 bits (29), Expect = 0.002
Identities = 65/83 (78%), Gaps = 0/83 (0%)
Strand=Plus/Plus

Query	1101	CCCTAGAGTAAACCTTAAGGTTCAACAACCAATAGAAATCACTCATTTTCACAGTTGATAT	1160
Sbjct	4129	CCCTAAAGTGAACCTCTACATTCAACCACCAATAGGAATTAGTTAATTGAGATTTGATAT	4188
Query	1161	CTTTTAAAAAAGTAAACAAAATA	1183
Sbjct	4189	CTTTTAAAAAATGAAACCAAATA	4211

Score = 56.4 bits (29), Expect = 0.002
Identities = 49/59 (83%), Gaps = 0/59 (0%)
Strand=Plus/Plus

Query	1595	GGTTTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTT	1653
Subject	4673	GGTTCAGGCTTTCCCCAAGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTT	4731

Group 4

Score = 56.4 bits (29), Expect = 0.002
Identities = 35/38 (92%), Gaps = 0/38 (0%)
Strand=Plus/Plus

```
Query 1523 TTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTT 1560
      ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4715 TTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTAGTATTT 4752
```

Score = 56.4 bits (29), Expect = 0.002
Identities = 58/70 (82%), Gaps = 1/70 (1%)
Strand=Plus/Plus

```
Query 544 TTTACCCAATGGTTCTGGATTTACCCAAGGGTTCCGGATTTAGGATTCAAGGTTTAGAGT 603
      ||||| ||||| || ||||| ||||| || ||||| || ||||| ||
Sbjct 88892 TTTACCCAAAGGTTTAGGGTTTAGGGTTTAGGGTTTAGGATT-AGAGTTTAGGGT 88950

Query 604 TTAGGATTTT 613
      ||||| |||||
Sbjct 88951 TTAGTATTTT 88960
```

Score = 56.4 bits (29), Expect = 0.002
Identities = 35/38 (92%), Gaps = 0/38 (0%)
Strand=Plus/Minus

```
Query 3838 GATAACCCGTTTAAATTATTTTCAAATTTTAAATTT 3875
      ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 133224 GATAACCCGTTTAAATTATTTTAAATTTTAAATTT 133187
```

Score = 54.5 bits (28), Expect = 0.008
Identities = 36/40 (90%), Gaps = 0/40 (0%)
Strand=Plus/Plus

```
Query 1529 GTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTA 1568
      ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct 4565 GTTTAGGGTTTAGGGTTTCGTGTTTAGAATTTAGGGTTTA 4604
```

Score = 52.6 bits (27), Expect = 0.031
Identities = 47/57 (82%), Gaps = 0/57 (0%)
Strand=Plus/Minus

```
Query 1121 TTCACCAACCAATAGAAATCACTCATTTACAGTTGATATCTTTTAAAAAGTAAAC 1177
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 4909 TTCACCCACCAATAGAAATTAGTTAATTAAGATTTGATATCTTTTAAAAAGGAAAC 4853
```

Group 4

Score = 52.6 bits (27), Expect = 0.031
Identities = 38/41 (92%), Gaps = 1/41 (2%)
Strand=Plus/Minus

```
Query 1281 TCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCCT 1321
          ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 88965 TCAACAAAATACTAAACCCTAAACTCT-AATCCTAAACCCT 88926
```

Score = 50.7 bits (26), Expect = 0.12
Identities = 45/52 (86%), Gaps = 1/52 (1%)
Strand=Plus/Minus

```
Query 1287 AAACACTAAACTCTAAACTCTAAATCCTAAACCCTTGGATAAATACTAAACC 1338
          |||| ||||| ||||| | ||||| ||||| ||||| ||||| |||||
Sbjct 88952 AAACCCTAAACTCTAATC-CTAAACCCTAAACCCTTGGGTAAACCCTAAACC 88902
```

Score = 48.8 bits (25), Expect = 0.45
Identities = 46/54 (85%), Gaps = 1/54 (1%)
Strand=Plus/Minus

```
Query 1523 TTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG 1576
          ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct 4507 TTTAGGATTTAGGGTTTAGTATT-AGGGGTTATAATTTAGGGTTTAGGGATTAG 4455
```

Score = 48.8 bits (25), Expect = 0.45
Identities = 27/28 (96%), Gaps = 0/28 (0%)
Strand=Plus/Plus

```
Query 1613 GGGTTTAGGGTTTAGGATTTAGGGTTTA 1640
          ||||| ||||| ||||| ||||| |||||
Sbjct 4719 GGGTTTAGGGTTTAGGGTTTAGGGTTTA 4746
```

Score = 48.8 bits (25), Expect = 0.45
Identities = 57/68 (83%), Gaps = 2/68 (2%)
Strand=Plus/Minus

```
Query 3450 ATTATAATATTATTATATTACTAATTGCAAAAATTAATTAATACATTATTTTAT-AATAA 3508
          |||| |||| ||||| ||||| |||| | ||| ||||| ||||| ||||| ||||
Sbjct 80053 ATTAAAATAACATTATATTTCTAATCACGAAA-TTAATTAATACATTATCTTATAAACAA 79995
```

```
Query 3509 ATATTTAA 3516
          |||||
Sbjct 79994 ATATTTAA 79987
```


Group 4

Score = 48.8 bits (25), Expect = 0.45
Identities = 38/42 (90%), Gaps = 1/42 (2%)
Strand=Plus/Minus

```
Query 3087      TAACAACATATTCATAGATTTTGTTT-ATCACTTGTTCTGTG 3127
                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 159562    TAACAACAGTTTCATAGATTTTTTTTATCACTTGTTCTGTG 159521
```

Score = 46.8 bits (24), Expect = 1.7
Identities = 34/39 (87%), Gaps = 0/39 (0%)
Strand=Plus/Minus

```
Query 1524      TTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAG 1562
                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 4486      TTAGGGGTTATAATTTAGGGTTTAGGGATTAGGATTTAG 4448
```

Score = 46.8 bits (24), Expect = 1.7
Identities = 30/33 (90%), Gaps = 0/33 (0%)
Strand=Plus/Plus

```
Query 1451      TTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG 1483
                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 4715      TTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTAG 4747
```

Score = 46.8 bits (24), Expect = 1.7
Identities = 35/38 (92%), Gaps = 1/38 (2%)
Strand=Plus/Plus

```
Query 1589      TCCAAGGGTTTAGGGTATACCCAAGGGTTTAGGGTTTA 1626
                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 88878     TCCAAGGGTT-AGGGTTTACCCAAAGGGTTTAGGGTTTA 88914
```

Score = 46.8 bits (24), Expect = 1.7
Identities = 28/30 (93%), Gaps = 0/30 (0%)
Strand=Plus/Plus

```
Query 1292      CTAAACTCTAAACTCTAAATCCTAAACCCT 1321
                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 173166    CTAAACCCTAAACCCTAAATCCTAAACCCT 173195
```

Group 4

Score = 46.8 bits (24), Expect = 1.7
Identities = 44/54 (81%), Gaps = 0/54 (0%)
Strand=Plus/Plus

```
Query 1500      AGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTT 1553
               ||||| ||| | || ||||| ||||| ||||| ||||| |||||
Sbjct 173381    AGGGTTTAGTATTTATCCAAGGGTTTAGGATTTAGAGTTTAGAGTTTAGTGT 173434
```

Score = 46.8 bits (24), Expect = 1.7
Identities = 28/30 (93%), Gaps = 0/30 (0%)
Strand=Plus/Plus

```
Query 1526      AGGGTTTAGGATTTAGGGTTTAGGGTTTAG 1555
               ||||| ||||| ||||| |||||
Sbjct 173400    AGGGTTTAGGATTTAGAGTTTAGAGTTTAG 173429
```

Score = 44.9 bits (23), Expect = 6.5
Identities = 29/32 (90%), Gaps = 0/32 (0%)
Strand=Plus/Minus

```
Query 1452      TTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG 1483
               ||||| ||| ||||| ||||| |||||
Sbjct 4486      TTAGGGGTTATAATTTAGGGTTTAGGGATTAG 4455
```

Score = 44.9 bits (23), Expect = 6.5
Identities = 47/59 (79%), Gaps = 0/59 (0%)
Strand=Plus/Plus

```
Query 1438      ATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAATTAT 1496
               |||| | || ||||| ||||| || | ||||| ||||| ||||| |||||
Sbjct 4553      ATTTGTCAAAGAGTTTAGGGTTTAGGGTTTCGTGTTTAGAATTTAGGGTTTAATATTAT 4611
```

Score = 44.9 bits (23), Expect = 6.5
Identities = 27/29 (93%), Gaps = 0/29 (0%)
Strand=Plus/Plus

```
Query 1448      GGGTTTAGGGTTTAGAATTTAGGGTTTAG 1476
               ||||| ||||| ||||| |||||
Sbjct 4719      GGGTTTAGGGTTTAGGGTTTAGGGTTTAG 4747
```

Score = 44.9 bits (23), Expect = 6.5
Identities = 108/148 (72%), Gaps = 1/148 (0%)
Strand=Plus/Plus

Group 4

```

Query 3686 ACTAGGGGTGGGCGTTCGGGTACCTATTCGGGTTTCGGTTCGAGTCTATTCGGATTTCGG 3745
          ||||| |||| ||||| |||| ||||| ||||| || || |||| |||||
Sbjct 40546 ACTAGGCATGGGTATTCGGGGTCCCTAATCGGGTTTCGGTTTTA-TCCATTTCAGATTTCGG 40604

Query 3746 ATTTTGGGGTCAAAGATTTTAGCCCCATTCGGTTATTTCTAAATTACGGTTCGGGTTCG 3805
          |||| ||| || | | |||| ||||| || || ||| | ||||| ||
Sbjct 40605 TTTTTCGGGTTTATCAAAACCAGCCCTATTCGGATTATTTGAAAGTTCGGTTCGGGACCG 40664

Query 3806 GTTCGGATCCTTGCGGATTCGGTTCGGG 3833
          ||||| | | || ||||| |||||
Sbjct 40665 GTTCGGGTTTTATCGGGTTCGGGTCGGG 40692

```

Score = 44.9 bits (23), Expect = 6.5
 Identities = 33/38 (86%), Gaps = 0/38 (0%)
 Strand=Plus/Plus

```

Query 1287 AAACACTAAACTCTAAACTCTAAATCCTAAACCCTTGG 1324
          |||| ||||| |||| |||| ||||| |||||
Sbjct 173168 AAACCCTAAACCCTAAATCCTAAACCCTAAACCCTTGG 173205

```

- **SEQ 2 from 54-05A application against DNA SEQ 1 from Brown provisional No. 1 (60/305,026)**

Score = 1152 bits (599), Expect = 0.0
 Identities = 677/716 (94%), Gaps = 0/716 (0%)
 Strand=Plus/Plus

```

Query 1329 GGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC 1388
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 480 GGGCGATCTTAATTCTGCTCAAGACCTTTTACAGGAGATGATTTCTAGTGGTGTGTGCCC 539

Query 1389 TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAACTAAAAGA 1448
          | || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 540 TAATGTCGTTACTTGTAACTTTGCTGGACGGTCTCTGCGATCGCGGAACTAAAAGA 599

Query 1449 TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC 1508
          ||||| ||||| ||||| ||||| || || || ||||| ||| |
Sbjct 600 TGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTATGATGGACATTGATGCTACTCATGC 659

Query 1509 CTTCAATGGTGTGGAACCTGATGTTCAAACCTACAATATATTGATCAGCGGCTTGATCAA 1568
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 660 CTTCAATGGTGTGGAACCTGATGTTCAAACCTACAATATATTGATCAGCGGATTGATTAA 719

Query 1569 TGAAGGGAAGTTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT 1628
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 720 TGAAGGGAAGTTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT 779

```

Group 4

Query	1629	CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA	1688
Sbjct	780	CCCAGATACTGTTACCTATAGCTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGA	839
Query	1689	TGAGGCTACACAAATGTTTGATTGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGAC	1748
Sbjct	840	TGAGGCTACACAAATGTTTGATTGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGAC	899
Query	1749	CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT	1808
Sbjct	900	ATTTAACACACTCATTACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCT	959
Query	1809	TTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT	1868
Sbjct	960	TTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAATGCAATTACTTACATCACTTTGAT	1019
Query	1869	TTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGAT	1928
Sbjct	1020	TCGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGTCTCTAGACATTTTCCAGGAGATGAT	1079
Query	1929	TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG	1988
Sbjct	1080	TTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTGACTGGTTTATGGAG	1139
Query	1989	TAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATGAGTATGG	2044
Sbjct	1140	TAAAGAGGAACTAAAAAGGGCACTGGCAATGCTTGAGGAACTGCAGATGAGTATGG	1195

Score = 612 bits (318), Expect = 3e-171
 Identities = 420/471 (89%), Gaps = 0/471 (0%)
 Strand=Plus/Plus

Query	547	AATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCGAA	606
Sbjct	13	AATGTCGTAACCTTCACCACTGATGAACGGTCTTTGCCGCGAGGGTAGAGTTGTCGAG	72
Query	607	GCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTAT	666
Sbjct	73	GCCGTAGCTCTGCTTGATCGGATGGTAGAAGATGGTCTCCAGCCTAACCAGATTACTTAC	132
Query	667	GGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTG	726
Sbjct	133	GGAACAATTGTAGATGGGATGTGTAAGATGGGAGACACTGTGTCTGCATTGAATCTTCTG	192
Query	727	AGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATT	786
Sbjct	193	AGGAAGATGGAGGAGTTGAGCCACATCAAACCGGATGTGGTAATCTATAGTGCCATCATT	252
Query	787	GATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAA	846
Sbjct	253	GATGGCCTTTTGAAAGACGGACGTCATACCGATGCTCAAAATCTTTTCACTGAAATGCAA	312

Group 4

- **SEQ 2 from 54-05A application against DNA SEQ 2 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 3 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 4 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 5 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 6 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 7 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 8 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 9 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 10 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 11 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 12 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found

Group 4

- **SEQ 2 from 54-05A application against DNA SEQ 13 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 14 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 15 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 16 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 17 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 18 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 19 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 20 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 21 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 22 from Brown provisional No. 1 (60/305,026)**

Score = 2959 bits (1539), Expect = 0.0
Identities = 1883/2050 (91%), Gaps = 18/2050 (0%)
Strand=Plus/Plus

Group 4

Query	1555	AGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCC	1614
Sbjct	1549	TGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCA	1608
Query	1615	CACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAG	1674
Sbjct	1609	CACAGAGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGACTATGCAAG	1668
Query	1675	CAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCT	1734
Sbjct	1669	CAGAGCCGCCTAGATGAGGCTACACAAATGTTTGTTTCGATGGGTAGCAAGAGCTTCTCT	1728
Query	1735	CCAAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGAT	1794
Sbjct	1729	CCCAACGTAGTGACATTTAACACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGAT	1788
Query	1795	GATGGGCTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACT	1854
Sbjct	1789	GATGGGCTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTGATGCAATTATT	1848
Query	1855	TACATCACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATT	1914
Sbjct	1849	TACATCACTTTGATTTATGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATT	1908
Query	1915	TTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTG	1974
Sbjct	1909	TTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTG	1968
Query	1975	ACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAG	2034
Sbjct	1969	ACTGGTTTTTGGAGTAAAGAGGAACTAGAAAGGGCAGTGGCAATGCTTGAGGATCTGCAG	2028
Query	2035	ATGAGTATGG	2044
Sbjct	2029	ATGAGTGTGG	2038

- **SEQ 2 from 54-05A application against DNA SEQ 23 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 24 from Brown provisional No. 1 (60/305,026)**

Score = 3930 bits (2044), Expect = 0.0
 Identities = 2044/2044 (100%), Gaps = 0/2044 (0%)
 Strand=Plus/Plus

Query	1	ATGTTGGCTAGGGTTTGTGGATTCAAGTGTCTCTTCTCTCTGCTGAGTCTGCGGCTAGA	60
Sbjct	250	ATGTTGGCTAGGGTTTGTGGATTCAAGTGTCTCTTCTCTCTGCTGAGTCTGCGGCTAGA	309

Group 4

Query	61	TTGTTCTGTACGAGATCGATTCTGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA	120
Sbjct	310	TTGTTCTGTACGAGATCGATTCTGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA	369
Query	121	GCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA	180
Sbjct	370	GCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA	429
Query	181	GAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT	240
Sbjct	430	GAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT	489
Query	241	GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT	300
Sbjct	490	GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT	549
Query	301	CTCTATCAGAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAATATTCTG	360
Sbjct	550	CTCTATCAGAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAATATTCTG	609
Query	361	ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCTTTGCTTTGTCTACATTTGGTAAGATC	420
Sbjct	610	ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCTTTGCTTTGTCTACATTTGGTAAGATC	669
Query	421	ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT	480
Sbjct	670	ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT	729
Query	481	GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGT	540
Sbjct	730	GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGT	789
Query	541	AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT	600
Sbjct	790	AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT	849
Query	601	GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT	660
Sbjct	850	GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT	909
Query	661	ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT	720
Sbjct	910	ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT	969
Query	721	CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA	780
Sbjct	970	CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA	1029
Query	781	ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA	840
Sbjct	1030	ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA	1089

Group 4

Query	841	ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTT	900
Sbjct	1090	ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTT	1149
Query	901	TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG	960
Sbjct	1150	TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG	1209
Query	961	ATCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAG	1020
Sbjct	1210	ATCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAG	1269
Query	1021	TTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACA	1080
Sbjct	1270	TTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACA	1329
Query	1081	ATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAG	1140
Sbjct	1330	ATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAG	1389
Query	1141	CACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACT	1200
Sbjct	1390	CACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACT	1449
Query	1201	CTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTCTCCATGAG	1260
Sbjct	1450	CTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTCTCCATGAG	1509
Query	1261	ATGACTGAAACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTCACGGGTTC	1320
Sbjct	1510	ATGACTGAAACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTCACGGGTTC	1569
Query	1321	TATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGT	1380
Sbjct	1570	TATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGT	1629
Query	1381	TTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAA	1440
Sbjct	1630	TTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAA	1689
Query	1441	CTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCT	1500
Sbjct	1690	CTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCT	1749
Query	1501	AGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTACAATATATTGATCAGCGGC	1560
Sbjct	1750	AGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTACAATATATTGATCAGCGGC	1809
Query	1561	TTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGG	1620
Sbjct	1810	TTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGG	1869

Group 4

Query	1621	GGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGC	1680
Sbjct	1870	GGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGC	1929
Query	1681	CGCCTAGATGAGGCTACACAAATGTTTGATTTCGATGGGTAGCAAGAGCTTCTCTCCAAAC	1740
Sbjct	1930	CGCCTAGATGAGGCTACACAAATGTTTGATTTCGATGGGTAGCAAGAGCTTCTCTCCAAAC	1989
Query	1741	GTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGG	1800
Sbjct	1990	GTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGG	2049
Query	1801	CTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACTTACATC	1860
Sbjct	2050	CTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACTTACATC	2109
Query	1861	ACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAG	1920
Sbjct	2110	ACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAG	2169
Query	1921	GAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGT	1980
Sbjct	2170	GAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGT	2229
Query	1981	TTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATGAGT	2040
Sbjct	2230	TTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATGAGT	2289
Query	2041	ATGG 2044	
Sbjct	2290	ATGG 2293	

- **SEQ 2 from 54-05A application against DNA SEQ 25 from Brown provisional No. 1 (60/305,026)**

Score = 1883 bits (979), Expect = 0.0
 Identities = 1104/1164 (94%), Gaps = 3/1164 (0%)
 Strand=Plus/Plus

Query	884	GTATGATAGTTGGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAG	943
Sbjct	779	GTATGATTAATGGATTTTGTAGCTCTGGTAGATGGAGTGAAGCCCAGCAGTTGTTGCAAG	838
Query	944	AAATGTTAGAAAGGAAGA---TCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATG	1000
Sbjct	839	AAATGTTAGAAAGGAAGAAGATCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATG	898
Query	1001	CATTTGTCAAGGAAGGCAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAA	1060
Sbjct	899	CATTTGTCAAGGAAGGCAAATTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAA	958

Group 4

Query	1061	GGGGTATAATCCCTAATACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGA	1120
Sbjct	959	GGGGTATAATCCCTAGTACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGA	1018
Query	1121	ATCGTCTTGATGCTGCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCA	1180
Sbjct	1019	ATCGTCTTGATGCTGCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGG	1078
Query	1181	ACCTAATCACTTTCAATACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATG	1240
Sbjct	1079	ACATAATCACTTTCAATACTCTCATAGCCGGATACTGTAGAGCTAAGAGGGTAGATGATG	1138
Query	1241	GAATGGAACCTTCTCCATGAGATGACTGAAACAGGATTAGTTGCTGACACAACCTACTTACA	1300
Sbjct	1139	GAATAAAACCTTCTCCATGAGATGACTGAAGCAGGATTAGTTGCTAACACAATTACTTACA	1198
Query	1301	ACACTCTTATTACGGGTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTAC	1360
Sbjct	1199	CCACTCTTATTACGGGTTCTGTGAGGTGGGCGATCTTAATGCTGCTCAAGACCTTCTAC	1258
Query	1361	AAGAGATGATCTCTAGTGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATG	1420
Sbjct	1259	AGGAGATGGTCTCTAGTGGTGTGTGCCCTAATGTCGTTACTTGTAACACTTTGCTGGACG	1318
Query	1421	GTCTCTGCGATAATGGGAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGA	1480
Sbjct	1319	GTCTCTGCGATAATGGGAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGA	1378
Query	1481	GTAAGAAGGATCTTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTT	1540
Sbjct	1379	GTAAGATGGATATTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTT	1438
Query	1541	ACAATATATTGATCAGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTAT	1600
Sbjct	1439	ACAATATATTGATCAGTGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTAT	1498
Query	1601	ACGAGGAGATGCCCCACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCG	1660
Sbjct	1499	ACGAGGAGATGCCACACAGAGGTATAGTCCCAGATACTATCACCTATAACTCAGTGATCC	1558
Query	1661	ATGGATTATGCAAGCAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTA	1720
Sbjct	1559	ATGGTTTATGCAAGCAAAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTA	1618
Query	1721	GCAAGAGCTTCTCTCAAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGG	1780
Sbjct	1619	GCAAGAGCTTCTCTCAAACGTAGTGACCTTTACTACACTCATTAATGGATACTGTAAGG	1678
Query	1781	CAGGAAGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTG	1840
Sbjct	1679	CAGGAAGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTG	1738

Group 4

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Query 1841 CTAACGCAATTACTTACATCACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATG 1900
          |||||||
Sbjct 1739 CTAACGCAATTACTTACATCACTTTGATTCATGGTTTTTCGTAAAGTGGGTAATATTAATG 1798

Query 1901 GGGCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCA 1960
          |||||||
Sbjct 1799 GGGCTCTAGATATTTTCCAGGAGATGATGGCAAGTGGTGTGTATCCTGATACCATTACTA 1858

Query 1961 TCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAAGTAAAAAGGGCAGTGGCAATGC 2020
          |||||||
Sbjct 1859 TCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAAGTAAAAAGGGCAGTGGCAATGC 1918

Query 2021 TTGAGAAACTGCAGATGAGTATGG 2044
          |||||
Sbjct 1919 TTGAGGATCTGCAGATGAGTGTGG 1942

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Score = 837 bits (435), Expect = 0.0
Identities = 663/772 (85%), Gaps = 15/772 (1%)
Strand=Plus/Plus

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Query 1 ATGTTGGCTAGGGTTTGTGGATTCAAGTGTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA 60
          |||||||
Sbjct 1 ATGTTGGCTAGGGTTTATAGATCCGGATCTTCTTCTTCTCCTGCTGTGTCTGCGGCTAGA 60

Query 61 TTGTTCTGTACGAGATCGATTTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA 120
          |||||||
Sbjct 61 TTGTTCTGTACGAGATCGATTTCGTGATGCTCTGGCCAAGAAAAGCAGGGA---TGGAGAG 117

Query 121 GCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA 180
          |||||||
Sbjct 118 AGTGGTTTTGGAGGAGAGAGTTTGAAGCTGCGAAGCGGATTTACGAAATCAAAGGGTTTA 177

Query 181 GAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT 240
          || ||
Sbjct 178 GAAGATGCGATTGATTTGTTTCGGTGATATGGTACGATCTCGTCCTTTACCTTCAGTAATT 237

Query 241 GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT 300
          |||||||
Sbjct 238 GATTTCTGTAAATTGATGGGAGTTGTGGTGAGGATGGGAAGGCTCGATGTTGTGATTTCT 297

Query 301 CTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTG 360
          ||| ||
Sbjct 298 CTCCATAGGAAGATGGAAATGAGGCGGGTTCCATGTAACGCATACAGCTTCACCATCCTG 357

Query 361 ATAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC 420
          || ||
Sbjct 358 ATGAAGTGTCTTCTGCAGCTGCTCTAAGCTGCCGTTTGTCTTGTCTACATTTGGTAAGATC 417

Query 421 ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT 480
          |||||||
Sbjct 418 ACCAAGCTTGGTTTTTCATCCCACTGTTGTTACCTTCAGCACCTGCTCCACGGATTATGT 477

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Group 4

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Query  481  GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTTCATCAAATGTTTGAAACGACATGT  540
          |||||  |||  |  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  478  GTGGAAGACAGGATCTCTGAAGCCTTGGATTTGTTTCATCAAATG-----TGT  525

Query  541  AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT  600
          |  ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  526  AAACCAAATGTCGTAACCTTCACCACGCTGATGAACGGTCTTTGCCGTGAGGGTCGAGTT  585

Query  601  GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT  660
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  586  GTCGAAGCTGTAGCTCTGCTTGATCGGATGCTAGAAGATGGTCTCCAGCCTAACCAGATT  645

Query  661  ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT  720
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  646  ACTTATGGAACAATCGTGGATGGGATGTGTAAGATGGGAGACACTGTGTCTGCATTGAAT  705

Query  721  CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCT  772
          ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  706  CTTCTGAGGAAGATGGAGGAGGTGAGCCACATCAAACCCAATGTGGTAATCT  757

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- **SEQ 2 from 54-05A application against DNA SEQ 26 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 27 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 28 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 29 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 30 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 31 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found

Group 4

- **SEQ 2 from 54-05A application against DNA SEQ 32 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 33 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 34 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 35 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 36 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 37 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 38 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 39 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 40 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 41 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against SEQ 1 from Brown provisional No. 2 (60/305,363)**

Score = 2961 bits (1540), Expect = 0.0
Identities = 1890/2060 (91%), Gaps = 18/2060 (0%)
Strand=Plus/Minus

Group 4

Query	1	ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA	60
Sbjct	4898	ATGTTGGCTAGGGTTTGCAGATTCGAGTCTTCTCCTTCTCGTCTTCTGTGTCTGCGGCTAGA	4839
Query	61	TTGTTCTGTACGAGATCGATTTCGTGATACTCTGGCCAAGGCAAGC-----GGAGAGAGT	114
Sbjct	4838	TTTTTCTGTACGGGATCGATTTCGTTCATGCTCTGGCCGAGAAAAGCAGGGATGGAGAGAGT	4779
Query	115	TGCGAAGCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAA	174
Sbjct	4778	GGCGAAGCAGGTTTTAGAGGAGAGAGTTTGAAGCTGCGAAGTGGATCTTATGAAATCAAA	4719
Query	175	GGTTTAGAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCT	234
Sbjct	4718	GGGTTAGAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCT	4659
Query	235	GTGGTTGATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTG	294
Sbjct	4658	GTGATTGATTTCAACAAGCTAATGGGTGCGGTGGTGAGAATGGAACGCCCGGATCTTGTG	4599
Query	295	ATTTCTCTCTATCAGAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAAT	354
Sbjct	4598	ATTTCTCTCTATCAAAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCACC	4539
Query	355	ATTCTGATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCCTTTGCTTTGTCTACATTTGGT	414
Sbjct	4538	ATTCTGATAAAATGTTTCTGCAGTTGCTCTAAGCTCCCCCTTTGCTTTGTCTACATTTGGT	4479
Query	415	AAGATCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGA	474
Sbjct	4478	AAGCTCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCACGGA	4419
Query	475	TTATGTGTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTTCATCAAATGTTTGAAACG	534
Sbjct	4418	TTATGTCTTGATCACAGGGTTTCTGAAGCCTTGGATTTGTTTCATCAAATTT-----	4367
Query	535	ACATGTAGGCCCAATGTCGTAACCTTCACCACCTTTGATGAACGGTCTTTGCCGCGAGGGT	594
Sbjct	4366	----GTAGACCAGATGTCCTAACGTTTACCACGCTGATGAATGGTCTTTGCCGCGAGGGT	4311
Query	595	AGAATTGTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACC	654
Sbjct	4310	CGAGTTGTCGAAGCCGTAGCTCTGCTTGATCGGATGGTGGAAAATGGTCTCCAGCCTGAC	4251
Query	655	CAGATTACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCA	714
Sbjct	4250	CAGATTACTTACGGAACATTTGTAGATGGGATGTGTAAGATGGGCGACACTGTGTCTGCA	4191
Query	715	CTGAATCTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTAT	774
Sbjct	4190	TTGAATCTTCTGAGGAAGATGGAGGAGATAAGCCACATCAAACCCAATGTGGTTATCTAT	4131

Group 4

Query	1555	AGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCC	1614
Sbjct	3350	TGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCA	3291
Query	1615	CACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAG	1674
Sbjct	3290	CACAGAGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGACTATGCAAG	3231
Query	1675	CAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCT	1734
Sbjct	3230	CAGAGCCGCCTAGATGAGGCTACACAAATGTTTGTTTCGATGGGTAGCAAGAGCTTCTCT	3171
Query	1735	CCAAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGAT	1794
Sbjct	3170	CCCAACGTAGTGACATTTAACACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGAT	3111
Query	1795	GATGGGCTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACT	1854
Sbjct	3110	GATGGGCTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTGATGCAATTATT	3051
Query	1855	TACATCACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATT	1914
Sbjct	3050	TACATCACTTTGATTTATGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATT	2991
Query	1915	TTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTG	1974
Sbjct	2990	TTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTG	2931
Query	1975	ACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAG	2034
Sbjct	2930	ACTGGTTTTTGGAGTAAAGAGGAACTAGAAAGGGCAGTGGCAATGCTTGAGGATCTGCAG	2871
Query	2035	ATGAGTATGGATCTATCATT	2054
Sbjct	2870	ATGAGTGTGGGTATGTCATT	2851

- **SEQ 2 from 54-05A application against SEQ 2 from Brown provisional No. 2 (60/305,363)**

Score = 3930 bits (2044), Expect = 0.0
 Identities = 2044/2044 (100%), Gaps = 0/2044 (0%)
 Strand=Plus/Minus

Query	1	ATGTTGGCTAGGGTTTGTGGATTCAAGTGTCTCTTCTCTCTGCTGAGTCTGCGGCTAGA	60
Sbjct	7150	ATGTTGGCTAGGGTTTGTGGATTCAAGTGTCTCTTCTCTCTGCTGAGTCTGCGGCTAGA	7091
Query	61	TTGTTCTGTACGAGATCGATTCTGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA	120
Sbjct	7090	TTGTTCTGTACGAGATCGATTCTGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA	7031

Group 4

Query	121	GCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA	180
Sbjct	7030	GCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA	6971
Query	181	GAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT	240
Sbjct	6970	GAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT	6911
Query	241	GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT	300
Sbjct	6910	GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT	6851
Query	301	CTCTATCAGAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAATATTCTG	360
Sbjct	6850	CTCTATCAGAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAATATTCTG	6791
Query	361	ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCTTTGCTTTGTCTACATTTGGTAAGATC	420
Sbjct	6790	ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCTTTGCTTTGTCTACATTTGGTAAGATC	6731
Query	421	ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT	480
Sbjct	6730	ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT	6671
Query	481	GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGT	540
Sbjct	6670	GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGT	6611
Query	541	AGGCCCAATGTCGTAACCTTCACCACCTTTCATGAACGGTCTTTGCCGCGAGGGTAGAATT	600
Sbjct	6610	AGGCCCAATGTCGTAACCTTCACCACCTTTCATGAACGGTCTTTGCCGCGAGGGTAGAATT	6551
Query	601	GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT	660
Sbjct	6550	GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT	6491
Query	661	ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT	720
Sbjct	6490	ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT	6431
Query	721	CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA	780
Sbjct	6430	CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA	6371
Query	781	ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA	840
Sbjct	6370	ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA	6311
Query	841	ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTT	900
Sbjct	6310	ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTT	6251

Group 4

Query	901	TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG	960
Sbjct	6250	TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG	6191
Query	961	ATCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAG	1020
Sbjct	6190	ATCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAG	6131
Query	1021	TTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACA	1080
Sbjct	6130	TTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACA	6071
Query	1081	ATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAG	1140
Sbjct	6070	ATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAG	6011
Query	1141	CACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACT	1200
Sbjct	6010	CACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACT	5951
Query	1201	CTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTCTCCATGAG	1260
Sbjct	5950	CTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTCTCCATGAG	5891
Query	1261	ATGACTGAAACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTCACGGGTTC	1320
Sbjct	5890	ATGACTGAAACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTCACGGGTTC	5831
Query	1321	TATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGT	1380
Sbjct	5830	TATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGT	5771
Query	1381	TTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAA	1440
Sbjct	5770	TTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAA	5711
Query	1441	CTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCT	1500
Sbjct	5710	CTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCT	5651
Query	1501	AGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTACAATATATTGATCAGCGGC	1560
Sbjct	5650	AGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTACAATATATTGATCAGCGGC	5591
Query	1561	TTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGG	1620
Sbjct	5590	TTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGG	5531
Query	1621	GGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGC	1680
Sbjct	5530	GGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGC	5471

Group 4

Query	1681	CGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAAC	1740
Sbjct	5470	CGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAAC	5411
Query	1741	GTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGG	1800
Sbjct	5410	GTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGG	5351
Query	1801	CTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACTTACATC	1860
Sbjct	5350	CTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACTTACATC	5291
Query	1861	ACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAG	1920
Sbjct	5290	ACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAG	5231
Query	1921	GAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGT	1980
Sbjct	5230	GAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGT	5171
Query	1981	TTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATGAGT	2040
Sbjct	5170	TTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATGAGT	5111
Query	2041	ATGG 2044	
Sbjct	5110	ATGG 5107	

Score = 1811 bits (942), Expect = 0.0
 Identities = 1046/1098 (95%), Gaps = 0/1098 (0%)
 Strand=Plus/Minus

Query	957	GAAGATCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGGAAGG	1016
Sbjct	14989	GAAGATCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGGAAGG	14930
Query	1017	CAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAA	1076
Sbjct	14929	CAAATTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAG	14870
Query	1077	TACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGC	1136
Sbjct	14869	TACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGC	14810
Query	1137	TGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAA	1196
Sbjct	14809	TGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGGACATAATCACTTTCAA	14750
Query	1197	TACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTCTCCA	1256
Sbjct	14749	TACTCTCATAGCCGGATACTGTAGAGCTAAGAGGGTAGATGATGGAATAAACTTCTCCA	14690

Group 4

Query	1257	TGAGATGACTGAAACAGGATTAGTTGCTGACACAACACTACTTACAACACTCTTATTACACGG	1316
Sbjct	14689	TGAGATGACTGAAGCAGGATTAGTTGCTAACACAATTACTTACACCACTCTTATTACACGG	14630
Query	1317	GTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAG	1376
Sbjct	14629	GTTCTGTCAGGTGGGCGATCTTAATGCTGCTCAAGACCTTCTACAGGAGATGGTCTCTAG	14570
Query	1377	TGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGG	1436
Sbjct	14569	TGGTGTGTGCCCTAATGTCGTTACTTGTAACTTTGCTGGACGGTCTCTGCGATAATGG	14510
Query	1437	GAAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGA	1496
Sbjct	14509	GAAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTAAGATGGATATTGA	14450
Query	1497	TGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTTACAATATATTGATCAG	1556
Sbjct	14449	TGCTAGTCACCCCTTTAATGGTGTGGAACCTGATGTTCAAACCTTACAATATATTGATCAG	14390
Query	1557	CGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCA	1616
Sbjct	14389	TGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCACA	14330
Query	1617	CAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCA	1676
Sbjct	14329	CAGAGGTATAGTCCCAGATACTATCACCTATAACTCAGTGATCCATGGTTTATGCAAGCA	14270
Query	1677	GAGCCGCCTAGATGAGGCTACACAAATGTTTGATTTCGATGGGTAGCAAGAGCTTCTCTCC	1736
Sbjct	14269	AAGCCGCCTAGATGAGGCTACACAAATGTTTGATTTCGATGGGTAGCAAGAGCTTCTCTCC	14210
Query	1737	AAACGTAGTGACCTTTACTACACTCATTAAATGGCTACTGTAAGGCAGGAAGGGTTGATGA	1796
Sbjct	14209	AAACGTAGTGACCTTTACTACACTCATTAAATGGATACTGTAAGGCAGGAAGGGTTGATGA	14150
Query	1797	TGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTA	1856
Sbjct	14149	TGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTA	14090
Query	1857	CATCACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTT	1916
Sbjct	14089	CATCACTTTGATTCATGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGATATTTT	14030
Query	1917	CCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGAC	1976
Sbjct	14029	CCAGGAGATGATGGCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTGAC	13970
Query	1977	TGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGAT	2036
Sbjct	13969	TGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGGATCTGCAGAT	13910



Group 4

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Query    2037      GAGTATGGATCTATCATT    2054
          ||||| ||| | | |||||
Sbjct    13909      GAGTGTGGGTATGTCATT    13892
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Score = 43.0 bits (22), Expect = 5.9
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

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Query    2043    GGATCTATCATTTGGGGGATGA    2064
          |||||
Sbjct    4981    GGATCTATCATTTGGGGGATGA    4960

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- **SEQ 2 from 54-05A application against SEQ 3 from Brown provisional No. 2 (60/305,363)**

Score = 2769 bits (1440), Expect = 0.0
Identities = 1858/2057 (90%), Gaps = 35/2057 (1%)
Strand=Plus/Minus

Query	1	ATGTTGGCTAGGGTTTGTGGATTCAAGTGTCTCTCTCTCCTGCTGAGTCTGCGGCTAGA	60
Sbjct	5916	ATGTTGGCTAGGGTTTATAGATCCGGATCTTCTCTCTCTCCTGCTGTGTCTGCGGCTAGA	5857
Query	61	TTGTTCTGTACGAGATCGATTTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA	120
Sbjct	5856	TTGTTCTGTACGAGATCGATTTCGTTCATGCTCTGGCCAAGAAAAGCAGGGA---TGGAGAG	5800
Query	121	GCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA	180
Sbjct	5799	AGTGGTTTTGGAGGAGAGAGTTTGAAGCTGCGAAGCGGATTTACGAAATCAAAGGGTTA	5740
Query	181	GAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT	240
Sbjct	5739	GAAGATGCGATTGATTTGTTTCGGTGATATGGTACGATCTCGTCCTTTACCTTCAGTAATT	5680
Query	241	GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT	300
Sbjct	5679	GATTTCTGTAAATTGATGGGAGTTGTGGTGAGGATGGGAAGGCTCGATGTTGTGATTTCT	5620
Query	301	CTCTATCAGAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAATATTCTG	360
Sbjct	5619	CTCCATAGGAAGATGGAAATGAGGCGGGTTCCATGTAACGCATACAGCTTCACCATCCTG	5560
Query	361	ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC	420
Sbjct	5559	ATGAAGTGTTTCTGCAGCTGCTCTAAGCTGCCGTTTGCTTTGTCTACATTTGGTAAGATC	5500
Query	421	ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT	480
Sbjct	5499	ACCAAGCTTGGTTTTTCATCCCACTGTTGTTACCTTCAGCACCCCTGCTCCACGGATTATGT	5440

Group 4

Query	481	GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGT	540
Sbjct	5439	GTGGAAGACAGGATCTCTGAAGCCTTGGATTTGTTTCATCAAATGTGTAAA-----	5389
Query	541	AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT	600
Sbjct	5388	---CCAAATGTCGTAACCTTCACCACGCTGATGAACGGTCTTTGCCGTGAGGGTCGAGTT	5332
Query	601	GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT	660
Sbjct	5331	GTCGAAGCTGTAGCTCTGCTTGATCGGATGCTAGAAGATGGTCTCCAGCCTAACCAGATT	5272
Query	661	ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT	720
Sbjct	5271	ACTTATGGAACAATCGTGGATGGGATGTGTAAGATGGGAGACACTGTGTCTGCATTGAAT	5212
Query	721	CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA	780
Sbjct	5211	CTTCTGAGGAAGATGGAGGAGGTGAGCCACATCAAACCCAATGTGGTAATCTG-----	5159
Query	781	ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA	840
Sbjct	5158	-----GCCTTTGGAAAGACGGACGTCATACCGATGCTCAAAATCTTTTCAGTGAA	5109
Query	841	ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTT	900
Sbjct	5108	ATGCAAGACAAGGGAATCTTTCCCAATTTATTTACCTACAGCTGTATGATTAATGGATTT	5049
Query	901	TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG	960
Sbjct	5048	TGTAGCTCTGGTAGATGGAGTGAAGCCCAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG	4989
Query	961	A---TCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGC	1017
Sbjct	4988	AAGATCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGC	4929
Query	1018	AAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAAT	1077
Sbjct	4928	AAATTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAGT	4869
Query	1078	ACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCT	1137
Sbjct	4868	ACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCT	4809
Query	1138	GAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAAT	1197
Sbjct	4808	GAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGGACATAATCACTTTCAAT	4749
Query	1198	ACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTCTCCAT	1257
Sbjct	4748	ACTCTCATAGCCGGATACTGTAGAGCTAAGAGGGTAGATGATGGAATAAACTTCTCCAT	4689

Group 4

Query	1258	GAGATGACTGAAACAGGATTAGTTGCTGACACAACACTACTTACAACACTCTTATTACAGGG	1317
Sbjct	4688	GAGATGACTGAAGCAGGATTAGTTGCTAACACAATTACTTACACCACTCTTATTACAGGG	4629
Query	1318	TTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGT	1377
Sbjct	4628	TTCTGTCAGGTGGGCGATCTTAATGCTGCTCAAGACCTTCTACAGGAGATGGTCTCTAGT	4569
Query	1378	GGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGG	1437
Sbjct	4568	GGTGTGTGCCCTAATGTCGTTACTTGTAACTTTGCTGGACGGTCTCTGCGATAATGGG	4509
Query	1438	AACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGAT	1497
Sbjct	4508	AACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTAAGATGGATATTGAT	4449
Query	1498	GCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTTACAATATATTGATCAGC	1557
Sbjct	4448	GCTAGTCACCCCTTTAATGGTGTGGAACCTGATGTTCAAACCTTACAATATATTGATCAGT	4389
Query	1558	GGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCAC	1617
Sbjct	4388	GGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCACAC	4329
Query	1618	AGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAG	1677
Sbjct	4328	AGAGGTATAGTCCCAGATACTATCACCTATAACTCAGTGATCCATGGTTTATGCAAGCAA	4269
Query	1678	AGCCGCCTAGATGAGGCTACACAAATGTTTGATTTCGATGGGTAGCAAGAGCTTCTCTCCA	1737
Sbjct	4268	AGCCGCCTAGATGAGGCTACACAAATGTTTGATTTCGATGGGTAGCAAGAGCTTCTCTCCA	4209
Query	1738	AACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGAT	1797
Sbjct	4208	AACGTAGTGACCTTTACTACACTCATTAATGGATACTGTAAGGCAGGAAGGGTTGATGAT	4149
Query	1798	GGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTAC	1857
Sbjct	4148	GGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTAC	4089
Query	1858	ATCACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTC	1917
Sbjct	4088	ATCACTTTGATTCATGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGATATTTTC	4029
Query	1918	CAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACT	1977
Sbjct	4028	CAGGAGATGATGGCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTGACT	3969
Query	1978	GGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATG	2037
Sbjct	3968	GGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGGATCTGCAGATG	3909

Group 4

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Query 1929 TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG 1988
          |||
Sbjct 1080 TTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTGACTGGTTTATGGAG 1139
          |||

Query 1989 TAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATGAGTATGG 2044
          |||
Sbjct 1140 TAAAGAGGAACTAAAAAGGGCACTGGCAATGCTTGAGGAACTGCAGATGAGTATGG 1195
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Score = 612 bits (318), Expect = 3e-171
 Identities = 420/471 (89%), Gaps = 0/471 (0%)
 Strand=Plus/Plus

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Query 547 AATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCGAA 606
          |||
Sbjct 13 AATGTCGTAACCTTCACCACGCTGATGAACGGTCTTTGCCGCGAGGGTAGAGTTGTCGAG 72
          |||

Query 607 GCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTAT 666
          |||
Sbjct 73 GCCGTAGCTCTGCTTGATCGGATGGTAGAAGATGGTCTCCAGCCTAACCAGATTACTTAC 132
          |||

Query 667 GGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTG 726
          |||
Sbjct 133 GGAACAATTGTAGATGGGATGTGTAAGATGGGAGACACTGTGTCTGCATTGAATCTTCTG 192
          |||

Query 727 AGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATT 786
          |||
Sbjct 193 AGGAAGATGGAGGAGTTGAGCCACATCAAACCGGATGTGGTAATCTATAGTGCCATCATT 252
          |||

Query 787 GATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAA 846
          |||
Sbjct 253 GATGGCCTTTGGAAAGACGGACGTCATACCGATGCTCAAAATCTTTTCACTGAAATGCAA 312
          |||

Query 847 GAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTGTAGC 906
          |||
Sbjct 313 GACAAGGGAATCTTTCCAGATATAGTTACCTACAGCTGTATGATTAATGGATTTTGTAGC 372
          |||

Query 907 TCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGC 966
          |||
Sbjct 373 TCTGGTAAATGGAGTGAAGCCCAGCGCTTGTGCAAGAAATGTTAGTAAGGAAGATCAGC 432
          |||

Query 967 CCTGATGTTGTAACCTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGC 1017
          |||
Sbjct 433 CCTGATGTTGTAACCTTTCAGTGGATTGATCAATGCATTGGTCAAAGAGGGC 483
          |||

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Score = 150 bits (78), Expect = 2e-32
 Identities = 316/435 (72%), Gaps = 0/435 (0%)
 Strand=Plus/Plus

Group 4

Query	967	CCTGATGTTGTAACCTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTT	1026
Sbjct	676	CCTGATGTTCAAACCTTACAATATATTGATCAGCGGATTGATTAATGAAGGGAAGTTTTTA	735
Query	1027	GAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACA	1086
Sbjct	736	GAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGTCCCAGATACTGTTACC	795
Query	1087	TATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATG	1146
Sbjct	796	TATAGCTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGATGAGGCTACACAAATG	855
Query	1147	TTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATA	1206
Sbjct	856	TTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGACATTTAACACACTCATT	915
Query	1207	GACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTCTCCATGAGATGACT	1266
Sbjct	916	ACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCTTTTCTGCGAGATGGGT	975
Query	1267	GAAACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTCACGGGTTCTATCTG	1326
Sbjct	976	CGAAGAGGGATAGTTGCTAATGCAATTACTTACATCACTTTGATTCGTGGTTTTTCGTAA	1035
Query	1327	GTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGC	1386
Sbjct	1036	GTGGGTAATATTAATGGGTCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTAT	1095
Query	1387	CCTGATATCGTTACT	1401
Sbjct	1096	CCTGATACCATTACT	1110

- **SEQ 2 from 54-05A application against DNA SEQ 2 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 3 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 4 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 5 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found

Group 4

- **SEQ 2 from 54-05A application against DNA SEQ 6 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 7 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 8 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 9 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 10 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 11 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 12 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 13 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 14 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 15 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 16 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found

Group 4

- **SEQ 2 from 54-05A application against DNA SEQ 17 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 18 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 19 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 20 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 21 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 22 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 23 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 24 from Brown provisional No. 3 (60/308,736)**

Score = 2959 bits (1539), Expect = 0.0
 Identities = 1883/2050 (91%), Gaps = 18/2050 (0%)
 Strand=Plus/Plus

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Query 1      ATGTTGGCTAGGGTTTGTGGATTCAAGTGTCTCTTCTCTCTGCTGAGTCTGCGGCTAGA 60
          |||
Sbjct 1      ATGTTGGCTAGGGTTTGCAGATTCGAGTCTTCTCTCTCTGCTCTTCTGTGTCTGCGGCTAGA 60

Query 61     TTGTTCTGTACGAGATCGATTTCGTGATACTCTGGCCAAGGCAAGC-----GGAGAGAGT 114
          ||
Sbjct 61     TTTTCTGTACGGGATCGATTTCGTGATGCTCTGGCCGAGAAAAGCAGGGATGGAGAGAGT 120

Query 115    TGCGAAGCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAA 174
          |||
Sbjct 121    GGCGAAGCAGGTTTTAGAGGAGAGAGTTTGAAGCTGCGAAGTGGATCTTATGAAATCAAA 180
  
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Group 4

Query	175	GGTTTAGAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCT	234
Sbjct	181	GGGTTAGAGGATGCGATTGATTTGTTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCT	240
Query	235	GTGGTTGATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTG	294
Sbjct	241	GTGATTGATTTCAACAAGCTAATGGGTGCGGTGGTGAGAATGGAACGCCCGGATCTTGTG	300
Query	295	ATTTCTCTCTATCAGAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAAT	354
Sbjct	301	ATTTCTCTCTATCAAAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAAC	360
Query	355	ATTCTGATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGT	414
Sbjct	361	ATTCTGATAAAATGTTTCTGCAGTTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGT	420
Query	415	AAGATCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGA	474
Sbjct	421	AAGCTCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCACGGA	480
Query	475	TTATGTGTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACG	534
Sbjct	481	TTATGTCTTGATCACAGGGTTTCTGAAGCCTTGGATTTGTTTCATCAAATTT-----	532
Query	535	ACATGTAGGCCCAATGTCGTAACCTTCACCCTTTGATGAACGGTCTTTGCCGCGAGGGT	594
Sbjct	533	----GTAGACCAGATGTCCTAACGTTTACCACGCTGATGAATGGTCTTTGCCGCGAGGGT	588
Query	595	AGAATTGTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACC	654
Sbjct	589	CGAGTTGTCGAAGCCGTAGCTCTGCTTGATCGGATGGTGGAAAATGGTCTCCAGCCTGAC	648
Query	655	CAGATTACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCA	714
Sbjct	649	CAGATTACTTACGGAACATTTGTAGATGGGATGTGTAAGATGGGCGACACTGTGTCTGCA	708
Query	715	CTGAATCTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTAT	774
Sbjct	709	TTGAATCTTCTGAGGAAGATGGAGGAGATAAGCCACATCAAACCCAATGTGGTTATCTAT	768
Query	775	AGTGCAATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTC	834
Sbjct	769	AGTGCCATCATTGATGGCCTTTGTAAAGATGGACGCCATAGCGATTCTCATAATCTTTTC	828
Query	835	ACTGAAATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTT	894
Sbjct	829	ATTGAAATGCAAGACAAGGGAATCTTTCCAAATATAGTTACCTACAACGTATGATCGGT	888
Query	895	GGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAA	954
Sbjct	889	GGATTTTGCATCTCTGGTAGATGGAGTGCAGCCCAGCGGTTGTTGCAAGAAATGTTAGAA	948

Group 4

Query	955	AGGAAGATCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGGAA	1014
Sbjct	949	AGGAAGATCAGCCCTAATGTTGTAACCTATAATGCTTTGATCAATGCATTTGTCAAGGAA	1008
Query	1015	GGCAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCT	1074
Sbjct	1009	GGCAAGTTCTTCGAGGCTGCAGAATTATACGATGAGATGCTTCCAAGGGGTATCATTCCCT	1068
Query	1075	AATACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCT	1134
Sbjct	1069	AATACAATCACATATAATTCAATGATCGATGGGTTTGCAAACAGGATCGTCTTGATGCT	1128
Query	1135	GCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTC	1194
Sbjct	1129	GCTGAGGACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGACGTATTCACCTTTC	1188
Query	1195	AATACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTCTC	1254
Sbjct	1189	ACTACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTCTC	1248
Query	1255	CATGAGATGACTGAAACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTCAC	1314
Sbjct	1249	CATGAGATGCCTAGAAGAGGATTAGTTGCTAACACAGTTACTTACAACACTCTTATTCAC	1308
Query	1315	GGGTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCT	1374
Sbjct	1309	GGGTTCTGTCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTCACAGCAGATGATTTCT	1368
Query	1375	AGTGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAAT	1434
Sbjct	1369	AGTGGTGTGTGCCCTGATATCGTTACTTGTAACTTTGCTGGACGGTCTCTGCGATAAT	1428
Query	1435	GGGAAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTT	1494
Sbjct	1429	GGGAAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTAAGATGGATCTT	1488
Query	1495	GATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTACAATATATTGATC	1554
Sbjct	1489	GATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCTAACTTACAATATATTGATC	1548
Query	1555	AGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCC	1614
Sbjct	1549	TGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCA	1608
Query	1615	CACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAG	1674
Sbjct	1609	CACAGAGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGACTATGCAAG	1668
Query	1675	CAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCT	1734
Sbjct	1669	CAGAGCCGCCTAGATGAGGCTACACAAATGTTTGTTTCGATGGGTAGCAAGAGCTTCTCT	1728

Group 4

Query	241	GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCCGGATCTTGTGATTTCT	300
Sbjct	490	GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCCGGATCTTGTGATTTCT	549
Query	301	CTCTATCAGAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAATATTCTG	360
Sbjct	550	CTCTATCAGAAGATGGAAAGGAAACAGATTTCGATGTGATATATACAGCTTCAATATTCTG	609
Query	361	ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC	420
Sbjct	610	ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC	669
Query	421	ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT	480
Sbjct	670	ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT	729
Query	481	GTGGAAGATAGGGTTTCTGAAGCCTTGATTTTTTTTCATCAAATGTTTGAAACGACATGT	540
Sbjct	730	GTGGAAGATAGGGTTTCTGAAGCCTTGATTTTTTTTCATCAAATGTTTGAAACGACATGT	789
Query	541	AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT	600
Sbjct	790	AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT	849
Query	601	GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT	660
Sbjct	850	GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT	909
Query	661	ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT	720
Sbjct	910	ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT	969
Query	721	CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA	780
Sbjct	970	CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA	1029
Query	781	ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA	840
Sbjct	1030	ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA	1089
Query	841	ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTT	900
Sbjct	1090	ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTT	1149
Query	901	TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG	960
Sbjct	1150	TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG	1209
Query	961	ATCAGCCCTGATGTTGTAACCTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAG	1020
Sbjct	1210	ATCAGCCCTGATGTTGTAACCTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAG	1269

Group 4

Query	1021	TTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACA	1080
Sbjct	1270	TTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACA	1329
Query	1081	ATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAG	1140
Sbjct	1330	ATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAG	1389
Query	1141	CACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACT	1200
Sbjct	1390	CACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACT	1449
Query	1201	CTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTCTCCATGAG	1260
Sbjct	1450	CTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACCTTCTCCATGAG	1509
Query	1261	ATGACTGAAACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTACGGGTTC	1320
Sbjct	1510	ATGACTGAAACAGGATTAGTTGCTGACACAACCTACTTACAACACTCTTATTACGGGTTC	1569
Query	1321	TATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGT	1380
Sbjct	1570	TATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGT	1629
Query	1381	TTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAA	1440
Sbjct	1630	TTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAA	1689
Query	1441	CTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCT	1500
Sbjct	1690	CTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCT	1749
Query	1501	AGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTTACAATATATTGATCAGCGGC	1560
Sbjct	1750	AGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTTACAATATATTGATCAGCGGC	1809
Query	1561	TTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGG	1620
Sbjct	1810	TTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGG	1869
Query	1621	GGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGC	1680
Sbjct	1870	GGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGC	1929
Query	1681	CGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCAAAC	1740
Sbjct	1930	CGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCAAAC	1989
Query	1741	GTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGG	1800
Sbjct	1990	GTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGG	2049

Group 4

Query	1801	CTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACTTACATC	1860
Sbjct	2050	CTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTGCTAACGCAATTACTTACATC	2109
Query	1861	ACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAG	1920
Sbjct	2110	ACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAG	2169
Query	1921	GAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGT	1980
Sbjct	2170	GAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGT	2229
Query	1981	TTATGGAGTAAAGAGGAAGTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATGAGT	2040
Sbjct	2230	TTATGGAGTAAAGAGGAAGTAAAAAGGGCAGTGGCAATGCTTGAGAACTGCAGATGAGT	2289
Query	2041	ATGG 2044	
Sbjct	2290	ATGG 2293	

- **SEQ 2 from 54-05A application against DNA SEQ 27 from Brown provisional No. 3 (60/308,736)**

Score = 1883 bits (979), Expect = 0.0
 Identities = 1104/1164 (94%), Gaps = 3/1164 (0%)
 Strand=Plus/Plus

Query	884	GTATGATAGTTGGTTTTTTGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAG	943
Sbjct	779	GTATGATTAATGGATTTTGTAGCTCTGGTAGATGGAGTGAAGCCCAGCAGTTGTTGCAAG	838
Query	944	AAATGTTAGAAAGGAAGA---TCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATG	1000
Sbjct	839	AAATGTTAGAAAGGAAGAAGATCAGCCCTGATGTTGTAACCTATAATGCTTTGATCAATG	898
Query	1001	CATTTGTCAAGGAAGGCAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAA	1060
Sbjct	899	CATTTGTCAAGGAAGGCAAATTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAA	958
Query	1061	GGGGTATAATCCCTAATACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGA	1120
Sbjct	959	GGGGTATAATCCCTAGTACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGA	1018
Query	1121	ATCGTCTTGATGCTGCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCA	1180
Sbjct	1019	ATCGTCTTGATGCTGCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGG	1078
Query	1181	ACCTAATCACTTTCAATACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATG	1240
Sbjct	1079	ACATAATCACTTTCAATACTCTCATAGCCGGATACTGTAGAGCTAAGAGGGTAGATGATG	1138

Group 4

Query	1241	GAATGGAACCTTCTCCATGAGATGACTGAAACAGGATTAGTTGCTGACACAACCTACTTACA	1300
Sbjct	1139	GAATAAAACCTTCTCCATGAGATGACTGAAGCAGGATTAGTTGCTAACACAATTACTTACA	1198
Query	1301	ACACTCTTATTACAGGGTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTAC	1360
Sbjct	1199	CCACTCTTATTACAGGGTTCTGTCTAGGTGGGCGATCTTAATGCTGCTCAAGACCTTCTAC	1258
Query	1361	AAGAGATGATCTCTAGTGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATG	1420
Sbjct	1259	AGGAGATGGTCTCTAGTGGTGTGTGCCCTAATGTCGTTACTTGTAACTTTGCTGGACG	1318
Query	1421	GTCTCTGCGATAATGGGAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGA	1480
Sbjct	1319	GTCTCTGCGATAATGGGAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGA	1378
Query	1481	GTAAGAAGGATCTTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTT	1540
Sbjct	1379	GTAAGATGGATATTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACCTT	1438
Query	1541	ACAATATATTGATCAGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTAT	1600
Sbjct	1439	ACAATATATTGATCAGTGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTAT	1498
Query	1601	ACGAGGAGATGCCCCACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCG	1660
Sbjct	1499	ACGAGGAGATGCCACACAGAGGTATAGTCCCAGATACTATCACCTATAACTCAGTGATCC	1558
Query	1661	ATGGATTATGCAAGCAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTTCGATGGGTA	1720
Sbjct	1559	ATGGTTTATGCAAGCAAAGCCGCCTAGATGAGGCTACACAAATGTTTGATTTCGATGGGTA	1618
Query	1721	GCAAGAGCTTCTCTCCAAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGG	1780
Sbjct	1619	GCAAGAGCTTCTCTCCAAACGTAGTGACCTTTACTACACTCATTAATGGATACTGTAAGG	1678
Query	1781	CAGGAAGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTG	1840
Sbjct	1679	CAGGAAGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCTGAAGAGGGATAGTTG	1738
Query	1841	CTAACGCAATTACTTACATCACTTTGATTTGTGGTTTTTCGTAAAGTGGGTAATATTAATG	1900
Sbjct	1739	CTAACGCAATTACTTACATCACTTTGATTCATGGTTTTTCGTAAAGTGGGTAATATTAATG	1798
Query	1901	GGGCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCA	1960
Sbjct	1799	GGGCTCTAGATATTTTCCAGGAGATGATGGCAAGTGGTGTGTATCCTGATACCATTACTA	1858
Query	1961	TCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGC	2020
Sbjct	1859	TCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGC	1918

Group 4

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Query 661 ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 646 ACTTATGGAACAATCGTGGATGGGATGTGTAAGATGGGAGACACTGTGTCTGCATTGAAT 705

Query 721 CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATAACCCAATGTTGTAATCT 772
          || ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 706 CTTCTGAGGAAGATGGAGGAGGTGAGCCACATCAAACCCAATGTGGTAATCT 757

```

- **SEQ 2 from 54-05A application against DNA SEQ 28 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 29 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 30 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 31 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 32 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 33 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 34 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 35 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 36 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found

Group 4

- **SEQ 2 from 54-05A application against DNA SEQ 37 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 38 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 39 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 40 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 41 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 42 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 2 from 54-05A application against DNA SEQ 43 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 1 from Brown provisional No. 1 (60/305,026)**

Score = 521 bits (1341), Expect = 2e-145

Identities = 261/395 (66%), Positives = 311/395 (78%), Gaps = 1/395 (0%)

Query	288	PDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEEL	347
		P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L	
Sbjct	4	PNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL	63
Query	348	YDEMLPRGII-PNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSNLTITNTLIDGYC	406
		+M I P+ + YS++IDG K R A+++F M KG P+++T++ +I+G+C	
Sbjct	64	LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC	123
Query	407	GAKRIDDGMELLHEMTETGLVADTTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIV	466
		+ + + LL EM + D T++ LI+ GDLN+A DLLQEMISSG+CP++V	
Sbjct	124	SSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNVV	183

Group 4

Query	467	TCDTLLDGLCDNGKLKDALEMFKVMQKSKKDL DASHFNGVEPDVQTYNILISGLINEGK	526
		TC+TLLDGLCD GKLKDALEMFK MQKS D+DA+H FNGVEPDVQTYNILISGLINEGK	
Sbjct	184	TCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEGK	243
Query	527	FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTF	586
		FLEAEELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLEATQMFDSMGSKSFSPN+VTF T	
Sbjct	244	FLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNT	303
Query	587	LINGYCKAGRVDGLELFCCEMGRRGIVANAITYITLICGFRKVGNGALDIFQEMISSG	646
		LI GYCKAG VDDGLELFCCEMGRRGIVANAITYITLI GFRKVGNG+LDIFQEMISSG	
Sbjct	304	LITGYCKAGMVDGLELFCCEMGRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISSG	363
Query	647	VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSM 681	
		VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSM	
Sbjct	364	VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSM 398	

Score = 394 bits (1012), Expect = 2e-107

Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

Query	180	CRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA	239
		C+PNVVTFTTLMNGLCREGR+VEAVALDRM+EDGLQP QITYGTIVDGMCK GDTVSA	
Sbjct	2	CKPNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSA	61
Query	240	NLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTQMKEGIFPDFTYNSMIVG	299
		NLLRKMEE+SHI P+VVIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G	
Sbjct	62	NLLRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMING	121
Query	300	FCSSGRWSDAEQLLQEMLERKISPDPVTYNALINAFVKEGKFFAEELYDEMLPRGIIPN	359
		FCSSG+WS+A++LLQEML RKISPDPVT++ LINA VKEG A++L EM+ G+ PN	
Sbjct	122	FCSSGKWSEAQRLLQEMLVRKISPDPVTFSGLLNALVKEGDLNSAQDLLQEMISSGVCPN	181
Query	360	TITYSSMIDGFCQNRLDAAEHMFYLM-----ATKGCSPNLITFNTLIDGYCGA	408
		+T ++++DG C + +L A MF M A G P++ T+N LI G	
Sbjct	182	VVTCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINE	241
Query	409	KRIDGMEELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIVTC	468
		+ + EL EM G+V DT TY+++I+G L+ A + M S P+IVT	
Sbjct	242	GKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTF	301
Query	469	DTLLDGLCDNGKLKDALEMFKVMQKSKKDL DASHFNGVEPDVQTYNILISGLINEGKFL	528
		+TL+ G C G + D LE+F M + G+ + TY LI G G	
Sbjct	302	NTLITGYCKAGMVDGLELFCCEMGR-----RGIVANAITYITLIRGFRKVGNGIN	350
Query	529	EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSM 572	
		+ ++++EM G+ PDTIT +M+ GL + L A M + +	
Sbjct	351	GSLDIFQEMISSGVYPDTITIRNMLTGLWSKEELKRALAMLEEL 394	

Group 4

Score = 300 bits (767), Expect = 6e-79

Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

```

Query 147 PDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVAL 206
          P+VVTFTTLL+GLC E RV EA+ +M E +PN +T+ T+++G+C+ G V A+ L
Sbjct 4 PNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 207 LDRMME-DGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNVVIYSAIIDS 265
          L +M E ++P + Y I+DG+ K G A NL +M++ I P++V YS +I+
Sbjct 64 LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQD-KGIFPDIVTYSCMINGF 122

Query 266 CKDGRHSDAQNLFTTEMQEKGIFPDFTYNSMIVGFCSSGRWSDAEQLLQEMLE----- 318
          C G+ S+AQ L EM + I PD+ T++ +I G + A+ LLQEM+
Sbjct 123 CSSGKWSEAQRLLQEMLVKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPCNV 182

Query 319 -----RKISPDVVTYNALINAFVKEG 339
          + PDV TYN LI+ + EG
Sbjct 183 VTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEG 242

Query 340 KFFEAEELYDEMLPRGIIPNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFN 399
          KF EAEELY+EM RGI+P+T+TYSSMI+G CKQ+RLD A MF M +K SPN++TFN
Sbjct 243 KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN 302

Query 400 TLIDGYCGAKRIDGMEELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISS 459
          TLI GYC A +DDG+EL EM G+VA+ TY TLI GF VG++N +LD+ QEMISS
Sbjct 303 TLITGYCKAGMVDDGLELFCMGRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISS 362

Query 460 GLCPDIVTCDTLLDGLCDNGKLDKDALEMFKVMQKS 494
          G+ PD +T +L GL +LK AL M + +Q S
Sbjct 363 GVYPDTITIRNMLTGLWSKEELKRALAMLEELQMS 397

```

Score = 216 bits (551), Expect = 7e-54

Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

```

Query 77 PSVVDVFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNILIKFCSCSKLPFALST 136
          P+VV F LM + R R ++L +M ++ + ++ ++ C AL+
Sbjct 4 PNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 137 FGKITKLG-LHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLC 195
          K+ +L + PDVV ++ ++ GL + R ++A + F +M + P++VT++ ++NG C
Sbjct 64 LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC 123

Query 196 REGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNV 255
          G+ EA LL M+ + P +T+ +++ + K+GD SA +LL++M S + PNV
Sbjct 124 SSGKWSEAQRLLQEMLVKISPDVVTFSGLINALVKEGDLNSAQDLLQEMIS-SGVCPCNV 182

Query 256 VIYSAIIDSCKDGRHSDAQNLFTTEMQ-----KGIFPDFTYNSMIVGFCSSG 304
          V + ++D LC G+ DA +F MQ+ G+ PD+ TYN +I G + G
Sbjct 183 VTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEG 242

```

Group 4

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Query 305  RWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEEELYDEMLPRGIIPNTITYS 364
          ++ +AE+L +EM R I PD VTY+++IN K+ + EA +++D M + PN +T++
Sbjct 243  KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN 302

Query 365  SMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHEMTET 424
          ++I G+CK +D +F M +G N IT+ TLI G+ I+ +++ EM +
Sbjct 303  TLITGYCKAGMVDDGLELFCMGRGIVANAITYITLIRGFRKVGNGSLDIFQEMISS 362

Query 425  GLVADTTTNTLIHGFYLVGDLNAAALDLLQEM 456
          G+ DT T ++ G + +L AL +L+E+
Sbjct 363  GVYPDTITIRNMLTGLWSKEELKRALAMLEEL 394

```

Score = 193 bits (491), Expect = 6e-47
 Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

```

Query 62  DAIDLFSDMLRSRPLPSVVDFFCKLMGVVVRMERPDLVISLYQKMER-KQIRCDIYSFNIL 120
          +A+ L M+ P+ + + ++ + +M ++L +KME I+ D+ ++ +
Sbjct 24  EAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEELSHIKPDVVIYSAI 83

Query 121 IKCFCSCKSLPFALSTFGKITKLGLHPDVVTFNTLLHGLCVEDRVSEALDFFHQMFETTC 180
          I + A + F ++ G+ PD+VT++ +++G C + SEA +M
Sbjct 84  IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFCSSGKWSEAQRLLQEMLVRKI 143

Query 181  RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN 240
          P+VVTF+ L+N L +EG + A LL M+ G+ P +T T++DG+C +G AL
Sbjct 144  SPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNVVTCNTLLDGLCDRGKLDKDALE 203

Query 241  LLRKME-----EVSH-----IIPNVVIYSAIIDS LCKDGRHSDAQNLFTMQEKGIFPDL 290
          + + M+ + +H + P+V Y+ +I L +G+ +A+ L+ EM +GI PD
Sbjct 204  MFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEGKFLEAEELYEEMPHRGIVPDT 263

Query 291  FTYNMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEEELYDE 350
          TY+SMI G C R +A Q+ M + SP++VT+N LI + K G + EL+ E
Sbjct 264  VTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNTLITGYCKAGMVDDGLELFC 323

Query 351  MLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKR 410
          M RGI+ N ITY ++I GF K ++ + +F M + G P+ IT ++ G +
Sbjct 324  MGRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISSGVYPDTITIRNMLTGLWSKEE 383

Query 411  IDDGMEELLHEM 421
          + + +L E+
Sbjct 384  LKRALAMLEEL 394

```

Score = 118 bits (296), Expect = 3e-24
 Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

```

Query 52  SGFHEIKGLEDAIDLFSDMLRSRPLPSVVDFFCKLMGVVVRMERPDLVISLYQKMERKQIR 111
          +GF +A L +ML + P VV F L+ +V+ + L Q+M +
Sbjct 120  NGFCSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVC 179

```

Group 4

```

Query 112  CDIYSFNILIKFCSCSKLPFALSTFGKITKL-----GLHPDVVTF TTLLHGLC 160
          ++ + N L+ C KL AL F + K G+ PDV T+ L+ GL
Sbjct 180  PNVVTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLI 239

Query 161  VEDRVSEALDFFHQMFETTCRPNVVTF TTLMNGLCREGRIVEAVALLDRMMEDGLQPTQI 220
          E + EA + + +M P+ VT+++++NGLC++ R+ EA + D M P +
Sbjct 240  NEGKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDMSGSKSFSPNIV 299

Query 221  TYGTIVDGMCKKGDTVSA LNLLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQNLFT E 280
          T+ T++ G CK G L L +M I+ N + Y +I K G + + ++F E
Sbjct 300  TFNTLITGYCKAGMVDDGLELFC EMGRRG-IVANAITYITLIRGFRKVG NINGS LDIFQE 358

Query 281  MQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKIS 322
          M G++PD T +M+ G S A +L+E+ +S
Sbjct 359  MISSGVYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVS 400

```

- **SEQ 3 from 54-05A application against PRT SEQ 2 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 3 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 4 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 5 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 6 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 7 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 8 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 9 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found

Group 4

- No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 10 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 11 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 12 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 13 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 14 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 15 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 16 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 17 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 18 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 19 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 20 from Brown provisional No. 1 (60/305,026)**

Group 4

- No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 21 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 22 from Brown provisional No. 1 (60/305,026)**

Score = 1179 bits (3049), Expect = 0.0

Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	58
		MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct	1	MLARVCRFESSSSSSVSAARFFCTGSIRHALAEKSRDGESGEAGFRGESLKLRSYSYEIK	60
Query	59	GLEDAIDLFSMDLRSRPLPSVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFN	118
		GLEDAIDLFSMDLRSRPLPSV+DF KLMG VVRMERPDLVISLYQKMERKQIRCDIYSF	
Sbjct	61	GLEDAIDLFSMDLRSRPLPSVIDFNKLMGAVVRMERPDLVISLYQKMERKQIRCDIYSFT	120
Query	119	ILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTFITLLHGLCVEDRVSEALDFFHQMFET	178
		ILIKCFCSCSKLPFALSTFGK+TKLGLHPDVVTFITLLHGLC++ RVSEALD FHQ+	
Sbjct	121	ILIKCFCSCSKLPFALSTFGKLTKLGLHPDVVTFITLLHGLCLDHRVSEALDLFHQI---	177
Query	179	TCRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA	238
		CRP+V+TFTTLMNGLCREGR+VEAVALDRM+E+GLQP QITYGT VDGMCCK GDTVSA	
Sbjct	178	-CRPDVLTFTTLMNGLCREGRVVEAVALDRMVENGLQPDQITYGTIVDGMCKMGDTVSA	236
Query	239	LNLLRKMEEVSHIIPNVVIYSIAIDSLCKDGRHSDAQNLFTQMKEGIFPDFTYNSMIV	298
		LNLLRKMEE+SHI PNVVIYSIAID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	
Sbjct	237	LNLLRKMEEISHIKPNVVIYSIAIDGLCKDGRHSDSHNLFIEQDKGIFPNIVTYNCMIG	296
Query	299	GFCSSGRWSDAEQLLQEMLERKISPVDVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	358
		GFC SGRWS A++LLQEMLERKISP+VVTYNALINAFVKEGKFFEA ELYDEMLPRGIIP	
Sbjct	297	GFCISGRWSAAQRLQEMLERKISPNVVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	356
Query	359	NTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELL	418
		NTITY+SMIDGFCKQ+RLDAE MFYLMATKGCSP++ TF TLIDGYCGAKRIDDGMELL	
Sbjct	357	NTITYNSMIDGFCKQDRDLAAEDMFYLMATKGCSPDVFTFTTLIDGYCGAKRIDDGMELL	416
Query	419	HEMTETGLVADTTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIVTCNTLLDGLCDN	478
		HEM GLVA+T TYNTLIHGF LVGDLNAAALDL Q+MISSG+CPDIVTC+TLLDGLCDN	
Sbjct	417	HEMPRRGLVANTVTYNTLIHGFCLVGDLNAAALDLSQQMISSGVCPDIVTCNTLLDGLCDN	476
Query	479	GKLKDALEMFKVMQKSKKDLASHPFNGVEPDVQTYNIIISGLINEGKFLEAEELYEEMP	538
		GKLKDALEMFK MQSK DLDASHPFNGVEPDV TYNILI GLINEGKFLEAEELYEEMP	
Sbjct	477	GKLKDALEMFKAMQSKMDLDASHPFNGVEPDVLTYNILICGLINEGKFLEAEELYEEMP	536
Query	539	HRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFITTLINGYCKAGRVD	598
		HRGIVPDTITYSSMIDGLCKQSRLEATQMF SMGSKSFSPNVVTF TLINGYCKAGRVD	
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLEATQMFVSMGSKSFSPNVVTFITTLINGYCKAGRVD	596

Group 4

Query	599	DGLELFCCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	658
		DGLELFCCEMGRRGIVA+AI YITLI GFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	
Sbjct	597	DGLELFCCEMGRRGIVADAIYITLIYGFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	656
Query	659	TGLWSKEELKRAVAMLEKLQMSM	681
		TG WSKEEL+RAVAMLE LQMS+	
Sbjct	657	TGFWSKEELERAVAMLEDLQMSV	679

- **SEQ 3 from 54-05A application against PRT SEQ 23 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 24 from Brown provisional No. 1 (60/305,026)**

Score = 1368 bits (3541), Expect = 0.0
 Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	
Sbjct	84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143
Query	61	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	120
		EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	
Sbjct	144	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	203
Query	121	IKCFCSCKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	180
		IKCFCSCKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	
Sbjct	204	IKCFCSCKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	263
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	240
		RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	
Sbjct	264	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	323
Query	241	LLRKMEEVSHIIPNVVIYS AIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIVGF	300
		LLRKMEEVSHIIPNVVIYS AIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIVGF	
Sbjct	324	LLRKMEEVSHIIPNVVIYS AIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIVGF	383
Query	301	CSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	360
		CSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	
Sbjct	384	CSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	443
Query	361	ITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE	420
		ITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE	
Sbjct	444	ITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE	503
Query	421	MTETGLVADTTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	480
		MTETGLVADTTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	
Sbjct	504	MTETGLVADTTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	563

Group 4

Query	481	LKDALEMFKVMQKSKKDL DASH PFNGVEPDVQTYN ILISGLINEGKFLEAEELYEEMPHR	540
		LKDALEMFKVMQKSKKDL DASH PFNGVEPDVQTYN ILISGLINEGKFLEAEELYEEMPHR	
Sbjct	564	LKDALEMFKVMQKSKKDL DASH PFNGVEPDVQTYN ILISGLINEGKFLEAEELYEEMPHR	623
Query	541	GIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSFSPNVVTF TT LINGYCKAGR VDDG	600
		GIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSFSPNVVTF TT LINGYCKAGR VDDG	
Sbjct	624	GIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSFSPNVVTF TT LINGYCKAGR VDDG	683
Query	601	LELFCEMGRRGIVANAITYIT LICGFRKVG NINGALDIFQEMISSGVY PDTITIRNMLTG	660
		LELFCEMGRRGIVANAITYIT LICGFRKVG NINGALDIFQEMISSGVY PDTITIRNMLTG	
Sbjct	684	LELFCEMGRRGIVANAITYIT LICGFRKVG NINGALDIFQEMISSGVY PDTITIRNMLTG	743
Query	661	LWSKEELKRAVAMLEKLQMSM	681
		LWSKEELKRAVAMLEKLQMSM	
Sbjct	744	LWSKEELKRAVAMLEKLQMSM	764

- SEQ 3 from 54-05A application against PRT SEQ 25 from Brown provisional No. 1 (60/305,026)**

Score = 974 bits (2517), Expect = 0.0
 Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRS GFHEIKGL	59
Query	61	EDAIDLFS DMLRSRPLSPVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNIL	120
		EDAIDL F DM+RSRPLSPV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct	60	EDAIDLFGDMVR SRPLSPVIDFCKLMGVVVRMGR LDVVISLHRKMEMRRVPCNAYSFTIL	119
Query	121	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TTLLHGLCVEDRVSEALDFFHQMFETTC	180
		+KCFCSKSKLPFALSTFGKITKLGL FH	
Sbjct	120	MKCFCSCSKLPFALSTFGKITKLGL-----FH-----	145
Query	181	RPNVVTF TTLMNGLCREGRIVEAVAL LDRMMEDGLQPTQITYGTIVDGMCKKGDTV SALN	240
		P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+	
Sbjct	146	-PTVVTFTSTLLHGLCVEDRISEALDLFHQMCK---P NVVTF TTLMNGLCREGRVVEAVA	200
Query	241	LLRKMEEVSHIIPNVVIYS AIIDSLCKDGRHSDAQNLFT EMQKEG-IFPDLFTY-----N	294
		LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct	201	LLDRMLE-DGLQPNQITYGTIVDGMCKMGDTV SALNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	295	SMIVGFCSSGRWSDAEQLLQEMLERK-ISP DVVTYNALINAFVKEGKFFEAEELYDEMLP	353
		MI GFCSSGRWS+A+QLLQEMLERK ISP DVVTYNALINAFVKEGKFFEAEELYDEMLP	
Sbjct	260	CMINGFCSSGRWSEAQQLLQEMLERKKISP DVVTYNALINAFVKEGKFFEAEELYDEMLP	319
Query	354	RGIIPNTITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDD	413
		RGIIP+TITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD	
Sbjct	320	RGIIPSTITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSPDIITFNTLIAGYCRARVDD	379

Group 4

Query	414	GMELLHEMTETGLVADTTTTYNTLIHGFIYLVGDLNAAALDLLQEMISSGLCPDIVTCDTLLD	473
		G++LLHEMTE GLVA+T TY TLIHGF VGDLNAA DLLQEM+SSG+CP++VTC+TLLD	
Sbjct	380	GIKLLHEMTEAGLVANTITYTTLIHGFCQVGDLNAAQDLLQEMVSSGVCPCNVVTCNTLLD	439
Query	474	GLCDNGKLKDALEMFKVMQKSKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	533
		GLCDNGKLKDALEMFK MQKSK D+DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	
Sbjct	440	GLCDNGKLKDALEMFKAMQKSKMDIDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query	534	YEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFITTLINGYCK	593
		YEEMPHRGIVPDTITY+S+I GLCKQSRLEATQMFDSMGSKSFSPNVVTFITTLINGYCK	
Sbjct	500	YEEMPHRGIVPDTITYNSVIHGLCKQSRLEATQMFDSMGSKSFSPNVVTFITTLINGYCK	559
Query	594	AGRVDDGLELFCMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPDTIT	653
		AGRVDDGLELFCMGRRGIVANAITYITLI GFRKVGNGINGALDIFQEM++SGVYPDTIT	
Sbjct	560	AGRVDDGLELFCMGRRGIVANAITYITLIHGFRKVGNGINGALDIFQEMMASGVYPDTIT	619
Query	654	IRNMLTGLWSKEELKRAVAMLEKLQMSM	681
		IRNMLTGLWSKEELKRAVAMLE LQMS+	
Sbjct	620	IRNMLTGLWSKEELKRAVAMLEDLQMSV	647

- **SEQ 3 from 54-05A application against PRT SEQ 26 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 27 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 28 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 29 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 30 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 31 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found

Group 4

- **SEQ 3 from 54-05A application against PRT SEQ 32 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 33 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 34 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 35 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 36 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 37 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 38 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 39 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 40 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 41 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against SEQ 4 from Brown provisional No. 2 (60/305,363)**

Score = 1179 bits (3049), Expect = 0.0

Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

Group 4

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	58
Sbjct	1	MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	60
Query	59	GLEDAIDLFSMDLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFN	118
Sbjct	61	GLEDAIDLFSMDLRSRPLPSV+DF KLMG VVRMERPD LVISLYQKMERKQIRCDIYSF	120
Query	119	ILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFET	178
Sbjct	121	ILIKCFCSCSKLPFALSTFGK+TKLGLHPDVVTF TLLHGLC++ RVSEALD FHQ+	177
Query	179	TCRPNVVTF T TLMNGLCREGRIVEAVAL LDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA	238
Sbjct	178	CRP+V+TFT TLMNGLCREGR+VEAVAL LDRM+E+GLQP QITYGT V DGMCK GDTVSA	236
Query	239	LNLLRKMEEVSHIIPNVVIYS AIIDSLCKDGRHSDAQNLFT EMQEKGIFPD LFTYNSMIV	298
Sbjct	237	LNLLRKMEE+SHI PNVVIYS AIID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	296
Query	299	GFCSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFEA EELYDEMLPRGIIP	358
Sbjct	297	GFCISGRWSAAQRL LQEMLERKISP NVVTYNALINAFVKEGKFFEA EELYDEMLPRGIIP	356
Query	359	NTITYSSMIDGFCKQNR LDAAEHMFYLMATKGCS PN LITFNTLIDGYCGAKRIDDGMELL	418
Sbjct	357	NTITY+SMIDGFCKQ+RL DAAE MFYLMATKGCS P++ TF TLIDGYCGAKRIDDGMELL	416
Query	419	HEMTETGLVAD TTTTYNTLIHGFYLVGDLNAA LDLLQEMISSGLCPDIVTC DTL LDGLCDN	478
Sbjct	417	HEM GLVA+T TYNTLIHGF LVGDLNAA LD LQ+MISSG+CPDIVTC+TL LDGLCDN	476
Query	479	GKLKDALEMFKVMQKSKKDLDASH PFNGVEPDVQTYN ILISGLINEGKFLEAEELYEEMP	538
Sbjct	477	GKLKDALEMFK MQKSK DLDASH PFNGVEPDV TYNILI GLINEGKFLEAEELYEEMP	536
Query	539	HRGIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSFSPNVVTF T T LINGYCKAGRVD	598
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSR LDEATQMF SMGSKSFSPNVVTF T LINGYCKAGRVD	596
Query	599	DGLELFC EMGRRGIVANAITYIT LICGFRKVG NINGALDIFQEMISSGVYPDTITIRNML	658
Sbjct	597	DGLELFC EMGRRGIVA+AI YITLI GFRKVG NINGALDIFQEMISSGVYPDTITIRNML	656
Query	659	TGLWSKEELKRAVAMLEKLQMSM	681
Sbjct	657	TG WSKEEL+RAVAMLE LQMS+	679

- SEQ 3 from 54-05A application against SEQ 5 from Brown provisional No. 2 (60/305,363)

Group 4

Score = 1368 bits (3541), Expect = 0.0

Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
Sbjct	84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143
Query	61	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	120
Sbjct	144	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	203
Query	121	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	180
Sbjct	204	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	263
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	240
Sbjct	264	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	323
Query	241	LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTQMKEKGIFPDLFTYNSMIVGF	300
Sbjct	324	LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTQMKEKGIFPDLFTYNSMIVGF	383
Query	301	CSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	360
Sbjct	384	CSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	443
Query	361	ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCS PN LITFNTLIDGYCGAKRIDDGMELLHE	420
Sbjct	444	ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCS PN LITFNTLIDGYCGAKRIDDGMELLHE	503
Query	421	MTETGLVADTTTTYNTLIHGFYLVGDLNAA LDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	480
Sbjct	504	MTETGLVADTTTTYNTLIHGFYLVGDLNAA LDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	563
Query	481	LKDALEMFKVMQKSKKDL DASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	540
Sbjct	564	LKDALEMFKVMQKSKKDL DASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	623
Query	541	GIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSFSPNVVTFTTLINGYCKAGRVD DG	600
Sbjct	624	GIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSFSPNVVTFTTLINGYCKAGRVD DG	683
Query	601	LELFCEMGRRGIVANAITYITLICGRKVG NINGALDIFQEMISSGVYPDTITIRNMLTG	660
Sbjct	684	LELFCEMGRRGIVANAITYITLICGRKVG NINGALDIFQEMISSGVYPDTITIRNMLTG	743
Query	661	LWSKEELKRAVAMLEKLQMSM	681
Sbjct	744	LWSKEELKRAVAMLEKLQMSM	764

Group 4

- **SEQ 3 from 54-05A application against SEQ 6 from Brown provisional No. 2 (60/305,363)**

Score = 974 bits (2517), Expect = 0.0

Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSGFHEIKGL	59
Query	61	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNIL	120
		EDAIDLF DM+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct	60	EDAIDLFGDMVRSRPLPSVID FCKLMGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL	119
Query	121	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	180
		+KCFCSCSKLPFALSTFGKITKLGL FH	
Sbjct	120	MKCFCSCSKLPFALSTFGKITKLGL-----FH-----	145
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	240
		P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+	
Sbjct	146	-PTVVTFTSTLLHGLCVEDRISEALDLFHQMCK---P NVVTFTTLMNGLCREGRVVEAVA	200
Query	241	LLRKMEEVSHIIPNVVIYS AIIDSLCKDGRHSDAQNLFTQMKEG-IFPDLFTY-----N	294
		LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct	201	LLDRMLE-DGLQPNQITYGTIVDGMCKMGDTVSA LNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	295	SMIVGFCSSGRWSDAEQ LLQEMLERK-ISP DVVTYNALINAFVKEGKFFEAEEELYDEMLP	353
		MI GFCSSGRWS+A+Q LLQEMLERK ISP DVVTYNALINAFVKEGKFFEAEEELYDEMLP	
Sbjct	260	CMINGFCSSGRWSEAQ LLQEMLERKKISP DVVTYNALINAFVKEGKFFEAEEELYDEMLP	319
Query	354	RGIIPNTITYSSMIDGFCQ NR LDAAEHMFYLMATKGCS PNLITFNTLIDGYCGAKRID D	413
		RGIIP+TITYSSMIDGFCQ NR LDAAEHMFYLMATKGCS P++ITFNTLI GYC AKR+DD	
Sbjct	320	RGIIPSTITYSSMIDGFCQ NR LDAAEHMFYLMATKGCS PDIITFNTLIAGYCAKRVDD	379
Query	414	GMELLHEMTETGLVADTTTYNTLIHG FYLVGDLNAA DLLQEMISSGLCPDIVTCDTLLD	473
		G++LLHEMTE GLVA+T TY TLIHGF VGD LNAA DLLQEM+SSG+CP++VTC+TLLD	
Sbjct	380	GIKLLHEMTEAGLVANTITYTTLIHG FQCQVGD LNAAQDLLQEMVSSGVC PNVVTCNTLLD	439
Query	474	GLCDNGKLKDALEMFKVMQSKKDL DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	533
		GLCDNGKLKDALEMFK MQSK D+DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	
Sbjct	440	GLCDNGKLKDALEMFKAMQSKMDIDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query	534	YEEMPHRGIVPDTITYSSMIDGLCKQ SRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	593
		YEEMPHRGIVPDTITY+S+I GLCKQ SRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	
Sbjct	500	YEEMPHRGIVPDTITYNSVIHGLCKQ SRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	559
Query	594	AGRVDDGLELFCMGRRGIVANAITYITL ICGFRKVGNGINGALDIFQEMISSGVYPDTIT	653
		AGRVDDGLELFCMGRRGIVANAITYITLI GFRKVGNGINGALDIFQEM++SGVYPDTIT	
Sbjct	560	AGRVDDGLELFCMGRRGIVANAITYITLIHGFRKVGNGINGALDIFQEMMASGVYPDTIT	619

Group 4

Query 654 IRNMLTGLWSKEELKRAVAMLEKLQMSM 681
 IRNMLTGLWSKEELKRAVAMLE LQMS+
 Sbjct 620 IRNMLTGLWSKEELKRAVAMLEDLQMSV 647

- **SEQ 3 from 54-05A application against PRT SEQ 1 from Brown provisional No. 3 (60/308,736)**

Score = 521 bits (1341), Expect = 2e-145
 Identities = 261/395 (66%), Positives = 311/395 (78%), Gaps = 1/395 (0%)

Query 288 PDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPVDVVTYNALINAFVKEGKFFFEAEEL 347
 P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L
 Sbjct 4 PNVVTFITLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 348 YDEMLPRGII-PNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYC 406
 +M I P+ + YS++IDG K R A+++F M KG P+++T++ +I+G+C
 Sbjct 64 LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC 123

Query 407 GAKRIDDGMELLHEMTETGLVADTTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIV 466
 + + + LL EM + D T++ LI+ GDLN+A DLLQEMISSG+CP++V
 Sbjct 124 SSGKWSEAQRLLQEMLVKRISPVDVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNVV 183

Query 467 TCDTLLDGLCDNGKLKDALEMFKVMQKSKKDLDAHPFNGVEPDVQTYNILISGLINEGK 526
 TC+TLLDGLCD GKLKDALEMFK MQKS D+DA+H FNGVEPDVQTYNILISGLINEGK
 Sbjct 184 TCNTLLDGLCDRGLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEGK 243

Query 527 FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFIT 586
 FLEAEELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLEATQMFDSMGSKSFSPN+VTF T
 Sbjct 244 FLEAEELYEEMPHRGIVPDTVITYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNT 303

Query 587 LINGYCKAGRVDGGLFCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSG 646
 LI GYCKAG VDDGGLFCEMGRRGIVANAITYITLI GFRKVGNGING+LDIFQEMISSG
 Sbjct 304 LITGYCKAGMVDDGGLFCEMGRRGIVANAITYITLIRGFRKVGNGINGSLDIFQEMISSG 363

Query 647 VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSM 681
 VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSM
 Sbjct 364 VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSM 398

Score = 394 bits (1012), Expect = 2e-107
 Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

Query 180 CRPNVVTFTITLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSAL 239
 C+PNVVTFTITLMNGLCREGR+VEAVALDRM+EDGLQP QITYGTIVDGMCK GDTVSAL
 Sbjct 2 CKPNVVTFTITLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSAL 61

Query 240 NLLRKMEEVSHIIPNVVIYSAIIDSCLKDGRHSDAQNLFTEMQEKGIFPDFTYNSMIVG 299
 NLLRKMEE+SHI P+VVIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G
 Sbjct 62 NLLRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMING 121

Group 4

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Query 300 FCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPN 359
          FCSSG+WS+A++LLQEML RKISPDVVT++ LINA VKEG A++L EM+ G+ PN
Sbjct 122 FCSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPN 181

Query 360 TITYSSMIDGFCKQNRDLAAEHMFYLM-----ATKGCSPNLITFNTLIDGYCGA 408
          +T ++++DG C + +L A MF M A G P++ T+N LI G
Sbjct 182 VVTCNTLLDGLCDRGKCLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINE 241

Query 409 KRIDDGMELLHEMTETGLVADTTTYNTLIHGfYLVGDLNAALDLLQEMISSGLCPDIVTC 468
          + + EL EM G+V DT TY+++I+G L+ A + M S P+IVT
Sbjct 242 GKFLAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTF 301

Query 469 DTLLDGLCDNGKCLKDALEMFKVMQKSKKDL DASHFNGVEPDVQTYNILISGLINEGKFL 528
          +TL+ G C G + D LE+F M + G+ + TY LI G G
Sbjct 302 NTLITGYCKAGMVDDGLELFCMGR-----RGIVANAITYITLIRGFRKVGNNIN 350

Query 529 EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSM 572
          + ++++EM G+ PDTIT +M+ GL + L A M + +
Sbjct 351 GSLDIFQEMISSGVYPDTITIRNMLTGLWSKEELKRALAMLEEL 394

```

Score = 300 bits (767), Expect = 6e-79

Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

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Query 147 PDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCTRPNVVFTTTLMNGLCREGRIVEAVAL 206
          P+VVTFTTL++GLC E RV EA+ +M E +PN +T+ T+++G+C+ G V A+ L
Sbjct 4 PNVVFTTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 207 LDRMME-DGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNVVIYSAIIDL 265
          L +M E ++P + Y I+DG+ K G A NL +M++ I P++V YS +I+
Sbjct 64 LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQD-KGIFPDIVTYSCMINGF 122

Query 266 CKDGRHSDAQNLFTMQEKGIFPDFTYNSMIVGFCSSGRWSDAEQLLQEMLE----- 318
          C G+ S+AQ L EM + I PD+ T++ +I G + A+ LLQEM+
Sbjct 123 CSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNV 182

Query 319 -----RKISPDVVTYNALINAFVKEG 339
          + PDV TYN LI+ + EG
Sbjct 183 VTCNTLLDGLCDRGKCLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEG 242

Query 340 KFFAEELYDEMLPRGIIPNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFN 399
          KF EAEELY+EM RGI+P+T+TYSSMI+G CKQ+RLD A MF M +K SPN++TFN
Sbjct 243 KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN 302

Query 400 TLIDGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLIHGfYLVGDLNAALDLLQEMISS 459
          TLI GYC A +DDG+EL EM G+VA+ TY TLI GF VG++N +LD+ QEMISS
Sbjct 303 TLITGYCKAGMVDDGLELFCMGRRGIVANAITYITLIRGFRKVGNNINGSGLDIFQEMISS 362

Query 460 GLCPDIVTCDTLLDGLCDNGKCLKDALEMFKVMQKS 494
          G+ PD +T +L GL +LK AL M + +Q S
Sbjct 363 GVYPDTITIRNMLTGLWSKEELKRALAMLEELQMS 397

```

Group 4

Score = 216 bits (551), Expect = 7e-54
Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

Query	77	PSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNILIKFCSCSKLPFALST	136
		P+VV F LM + R R ++L +M ++ + ++ ++ C AL+	
Sbjct	4	PNVVTFTTLMNGLCREGRVVEAVAL LDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL	63
Query	137	FGKITKL G-LHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETT CRPNVVTFTTLMNGLC	195
		K+ +L + PDVV ++ ++ GL + R ++A + F +M + P++VT++ ++NG C	
Sbjct	64	LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIE MQDKGIFPDIVTYSCMINGFC	123
Query	196	REGRIVEAVAL LDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNV	255
		G+ EA LL M+ + P +T+ +++ + K+GD SA +LL++M S + PNV	
Sbjct	124	SSGKWSEAQRLLQEMLVRKISP DVVTFSG LINALVKEGDLNSAQDLLQEMIS-SGVC PN	182
Query	256	VIYSAIIDS LCKDGRHSDAQNLFT EMQE-----KGIFPDLFTYNSMIVGFCSSG	304
		V + ++D LC G+ DA +F MQ+ G+ PD+ TYN +I G + G	
Sbjct	183	VTCNTLLDGLCDRGK LKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYN ILISGLINEG	242
Query	305	RWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFEA EELYDEMLPRGIIPNTITYS	364
		++ +AE+L +EM R I PD VTY+++IN K+ + EA +++D M + PN +T++	
Sbjct	243	KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSR LDEATQMFD SMGSKSFSPNIVTFN	302
Query	365	SMIDGFCKQNRLDAAEHMFYLMATKGCS PN LITFNTLIDGYCGAKRID DGMELLHEMTET	424
		++I G+CK +D +F M +G N IT+ TLI G+ I+ +++ EM +	
Sbjct	303	TLITGYCKAGMVDDGLELFC EMGRRGIVANAITYITLIRGFRKVG NINGS L DIFQEMISS	362
Query	425	GLVADTTTTYNTLIHGFYLVGDLNAALDLLQEM	456
		G+ DT T ++ G + +L AL +L+E+	
Sbjct	363	GVYPDTITIRNMLTGLWSKEELKRALAMLEEL	394

Score = 193 bits (491), Expect = 6e-47
Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

Query	62	DAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMER-KQIRCDIYSFNIL	120
		+A+ L M+ P+ + + ++ + +M ++L +KME I+ D+ ++ +	
Sbjct	24	EAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEELSHIKPDVVIYSAI	83
Query	121	IKFCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETT C	180
		I + A + F ++ G+ PD+VT++ +++G C + SEA +M	
Sbjct	84	IDGLWKDGRHTDAQNLFIE MQDKGIFPDIVTYSCMINGFCSSGKWSEAQRLLQEMLVRKI	143
Query	181	RPNVVTFTTLMNGLCREGRIVEAVAL LDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN	240
		P+VVTF+ L+N L +EG + A LL M+ G+ P +T T++DG+C +G AL	
Sbjct	144	SPDVVTFSG LINALVKEGDLNSAQDLLQEMISSGVC PN VVTCNTLLDGLCDRGK LKDALE	203

Group 4

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Query  241  LLRKME-----EVSH----IIPNVVIYSAIIDSLCKDGRHSDAQNLFTQMKEKGIFPDL  290
          + + M+          + +H      + P+V  Y+ +I  L  +G+  +A+ L+ EM  +GI PD
Sbjct  204  MFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEGKFLEAEELYEEMPHRGIVPDT  263

Query  291  FTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVITYNALINAFVKEGKFFAEELYDE  350
          TY+SMI G C   R  +A Q+   M  +  SP++VT+N LI  + K G   + EL+ E
Sbjct  264  VTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNTLITGYCKAGMVDDGLELFC  323

Query  351  MLPRGIIPNTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKR  410
          M  RGI+ N ITY ++I GF K   ++ +  +F  M + G  P+ IT  ++ G   +
Sbjct  324  MGRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISSGVYPDTITIRNMLTGLWSKEE  383

Query  411  IDDGMELLHEM  421
          +   + +L E+
Sbjct  384  LKRALAMLEEL  394

```

Score = 118 bits (296), Expect = 3e-24

Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

```

Query  52   SGFHEIKGLEDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIR  111
          +GF          +A L  +ML  +  P VV F  L+  +V+   +   L Q+M   +
Sbjct  120  NGFCSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVC  179

Query  112  CDIYSFNILIKFCSCSKLPFALSTFGKITKL-----GLHPDVVTFTTLLHGLC  160
          ++ + N L+   C   KL  AL  F  + K               G+ PDV T+  L+ GL
Sbjct  180  PNVVTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLI  239

Query  161  VEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQI  220
          E +   EA + + +M          P+ VT+++++NGLC++ R+ EA  + D M          P  +
Sbjct  240  NEGKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIV  299

Query  221  TYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTE  280
          T+ T++ G CK G       L L  +M          I+ N + Y  +I   K G  + + ++F E
Sbjct  300  TFNTLITGYCKAGMVDDGLELFCMGRRG-IVANAITYITLIRGFRKVGNGSLDIFQE  358

Query  281  MQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKIS  322
          M  G++PD T  +M+ G S          A  +L+E+   +S
Sbjct  359  MISSGVYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVS  400

```

- **SEQ 3 from 54-05A application against PRT SEQ 2 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 3 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found

Group 4

- **SEQ 3 from 54-05A application against PRT SEQ 4 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 5 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 6 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 7 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 8 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 9 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 10 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 11 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 12 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 13 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 14 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found

Group 4

- **SEQ 3 from 54-05A application against PRT SEQ 15 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 16 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 17 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 18 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 19 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 20 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 21 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 22 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 23 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 24 from Brown provisional No. 3 (60/308,736)**

Score = 1179 bits (3049), Expect = 0.0

Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

```
Query 1 MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK 58
        MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK
Sbjct 1 MLARVCRFESSSSSVSAARFFCTGSIRHALAEKSRDGESGEAGFRGESLKLRSYSYEIK 60
```

Group 4

Query	59	GLEDAIDLFSMDLRSRPLPSVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFN	118
Sbjct	61	GLEDAIDLFSMDLRSRPLPSV+DF KLMG VVRMERPDLVISLYQKMERKQIRCDIYSF	120
Query	119	ILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TTLLHGLCVEDRVSEALDFFHQMFET	178
Sbjct	121	ILIKCFCSCSKLPFALSTFGK+TKLGLHPDVVTF TTLLHGLC++ RVSEALD FHQ+	177
Query	179	TCRPNVVTFTTLMNGLCREGRIVEAVALLD RMEDGLQPTQITYGTIVDGMCKKGDTVSA	238
Sbjct	178	-CRPDVLTFTTLMNGLCREGRVVEAVALLD RMVENGLQPDQITYGTIVDGMCKKGDTVSA	236
Query	239	LNLLRKMEEVSHIIPNVVIYS AIIDSLCKDGRHSDAQNLFTMQEKGIFPDFTYNSMIV	298
Sbjct	237	LNLLRKMEE+SHI PNVVIYS AIID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	296
Query	299	GFCSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFEA EELYDEMLPRGIIP	358
Sbjct	297	GFCISGRWSAAQRLQEMLERKISP DVVTYNALINAFVKEGKFFEA EELYDEMLPRGIIP	356
Query	359	NTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCS PNLITFNTLIDGYCGAKRIDDGMELL	418
Sbjct	357	NTITY+SMIDGFCKQ+RLDAE MFYLMATKGCS P++ TF TLIDGYCGAKRIDDGMELL	416
Query	419	HEMTETGLVADTTTTYNTLIHGFYLVGDLN AALDLLQEMISSGLCPDIVTCDTLLDGLCDN	478
Sbjct	417	HEMPRRGLVANTVTYNTLIHGFCLVGD LNAALDLSQQMISSGVCPDIVTCNTLLDGLCDN	476
Query	479	GKLKDALEMFKVMQKSKDLDASHPFNGVEPDVQ TYNILISGLINEGKFLEAEELYEEMP	538
Sbjct	477	GKLKDALEMFK MQKSK DLDASHPFNGVEPDV TYNILI GLINEGKFLEAEELYEEMP	536
Query	539	HRGIVPDTITYSSMIDGLCKQSRLEATQMFDS MGSKSFSPNVVTF TTLLINGYCKAGRVD	598
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLEATQMF SMGSKSFSPNVVTF TLLINGYCKAGRVD	596
Query	599	DGLELFCMGRRGIVANAITYITLICGFRKVG NINGALDIFQEMISSGVYPDTITIRNML	658
Sbjct	597	DGLELFCMGRRGIVA+AI YITLI GFRKVG NINGALDIFQEMISSGVYPDTITIRNML	656
Query	659	TGLWSKEELKRAVAMLEKLQMSM	681
Sbjct	657	TG WSKEEL+RAVAMLE LQMS+	679

- **SEQ 3 from 54-05A application against PRT SEQ 25 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found

Group 4

- **SEQ 3 from 54-05A application against PRT SEQ 26 from Brown provisional No. 3 (60/308,736)**

Score = 1368 bits (3541), Expect = 0.0

Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	
Sbjct	84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143
Query	61	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNIL	120
		EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNIL	
Sbjct	144	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNIL	203
Query	121	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	180
		IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	
Sbjct	204	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	263
Query	181	RPNVVTFTTLMNGLCREGRIVEAVAL LDRMMEDGLQPTQITYGTIVDGMCKKGDTV SALN	240
		RPNVVTFTTLMNGLCREGRIVEAVAL LDRMMEDGLQPTQITYGTIVDGMCKKGDTV SALN	
Sbjct	264	RPNVVTFTTLMNGLCREGRIVEAVAL LDRMMEDGLQPTQITYGTIVDGMCKKGDTV SALN	323
Query	241	LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNL FTEMQEKGIFPDLFTYNSMIVGF	300
		LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNL FTEMQEKGIFPDLFTYNSMIVGF	
Sbjct	324	LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNL FTEMQEKGIFPDLFTYNSMIVGF	383
Query	301	CSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKF FEAEEELYDEMLPRGIIPNT	360
		CSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKF FEAEEELYDEMLPRGIIPNT	
Sbjct	384	CSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKF FEAEEELYDEMLPRGIIPNT	443
Query	361	ITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE	420
		ITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE	
Sbjct	444	ITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE	503
Query	421	MTETGLVADTTTYNTLIHG FYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	480
		MTETGLVADTTTYNTLIHG FYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	
Sbjct	504	MTETGLVADTTTYNTLIHG FYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	563
Query	481	LKDALEMFKVMQSKSKDL DASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	540
		LKDALEMFKVMQSKSKDL DASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	
Sbjct	564	LKDALEMFKVMQSKSKDL DASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	623
Query	541	GIVPDTITYSSMIDGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVD DG	600
		GIVPDTITYSSMIDGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVD DG	
Sbjct	624	GIVPDTITYSSMIDGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVD DG	683
Query	601	LELFCEMGRRGIVANAITYIT LICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNMLTG	660
		LELFCEMGRRGIVANAITYIT LICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNMLTG	
Sbjct	684	LELFCEMGRRGIVANAITYIT LICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNMLTG	743

Group 4

Query 661 LWSKEELKRAVAMLEKLQMSM 681
LWSKEELKRAVAMLEKLQMSM
Sbjct 744 LWSKEELKRAVAMLEKLQMSM 764

- **SEQ 3 from 54-05A application against PRT SEQ 27 from Brown provisional No. 3 (60/308,736)**

Score = 974 bits (2517), Expect = 0.0

Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSFGFHEIKGL	59
Query	61	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	120
		EDAIDLF DM+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct	60	EDAIDLFGDMVRSRPLPSVID FCKLMGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL	119
Query	121	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	180
		+KCFCSCSKLPFALSTFGKITKLG FH	
Sbjct	120	MKCFCSCSKLPFALSTFGKITKLG-----FH-----	145
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	240
		P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+	
Sbjct	146	-PTVVTFTSTLLHGLCVEDRISEALDLFHQMCK---P NVVTFTTLMNGLCREGRVVEAVA	200
Query	241	LLRKMEEVSHIIPNVVIYS AIIDSLCKDGRHSDAQNLFTMQEKG-IFPDLFTY-----N	294
		LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct	201	LLDRMLE-DGLQPNQITYGTIVDGMCKMGDTVSA LNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	295	SMIVGFCSSGRWSDAEQLLQEMLERK-ISP DVVTYNALINAFVKEGKFFAEELYDEMLP	353
		MI GFCSSGRWS+A+QLLQEMLERK ISP DVVTYNALINAFVKEGKFFAEELYDEMLP	
Sbjct	260	CMINGFCSSGRWSEAAQLLQEMLERKKISP DVVTYNALINAFVKEGKFFAEELYDEMLP	319
Query	354	RGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDD	413
		RGIIP+TITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD	
Sbjct	320	RGIIPSTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPDIITFNTLIAGYCRAKRVDD	379
Query	414	GMELLHEMTETGLVADTTTYNTLIHG FYLVGDLNAA DLLQEMISSGLCPDIVTCDTLLD	473
		G++LLHEMTE GLVA+T TY TLIHGF VGDLNAA DLLQEM+SSG+CP++VTC+TLLD	
Sbjct	380	GIKLLHEMTEAGLVANTITYTTLIHGFCQVGDLNAAQDLLQEMVSSGVC PNVVTCNTLLD	439
Query	474	GLCDNGKLKDALEMFKVMQSKKDL DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	533
		GLCDNGKLKDALEMFK MQSK D+DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	
Sbjct	440	GLCDNGKLKDALEMFKAMQSKMDIDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query	534	YEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	593
		YEEMPHRGIVPDTITY+S+I GLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	
Sbjct	500	YEEMPHRGIVPDTITYNSVIHGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	559

Group 4

Query	594	AGRVDDGLELFCCEMGRRGIVANAITYITLICGFRKVGNGALDIFQEMISSGVYPDTIT	653
		AGRVDDGLELFCCEMGRRGIVANAITYITLI GFRKVGNGALDIFQEM++SGVYPDTIT	
Sbjct	560	AGRVDDGLELFCCEMGRRGIVANAITYITLIHGFRKVGNGALDIFQEMMASGVYPDTIT	619
Query	654	IRNMLTGLWSKEELKRAVAMLEKLQMSM	681
		IRNMLTGLWSKEELKRAVAMLE LQMS+	
Sbjct	620	IRNMLTGLWSKEELKRAVAMLEDLQMSV	647

- **SEQ 3 from 54-05A application against PRT SEQ 28 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 29 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 30 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 31 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 32 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 33 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 34 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 35 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 36 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found

Group 4

- **SEQ 3 from 54-05A application against PRT SEQ 37 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 38 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 39 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 40 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 41 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 42 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from 54-05A application against PRT SEQ 43 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found